

When using a probe to detect a specific target, the probe must be able to bind to the target. This is often achieved by using a probe that is complementary to the target. In this case, the probe is a single-stranded DNA molecule that is complementary to the target DNA sequence. The probe is labeled with a fluorescent marker, which allows it to be detected. When the probe binds to the target, the fluorescent marker is brought into close proximity with the target, resulting in a signal. This is the principle of fluorescence resonance energy transfer (FRET).

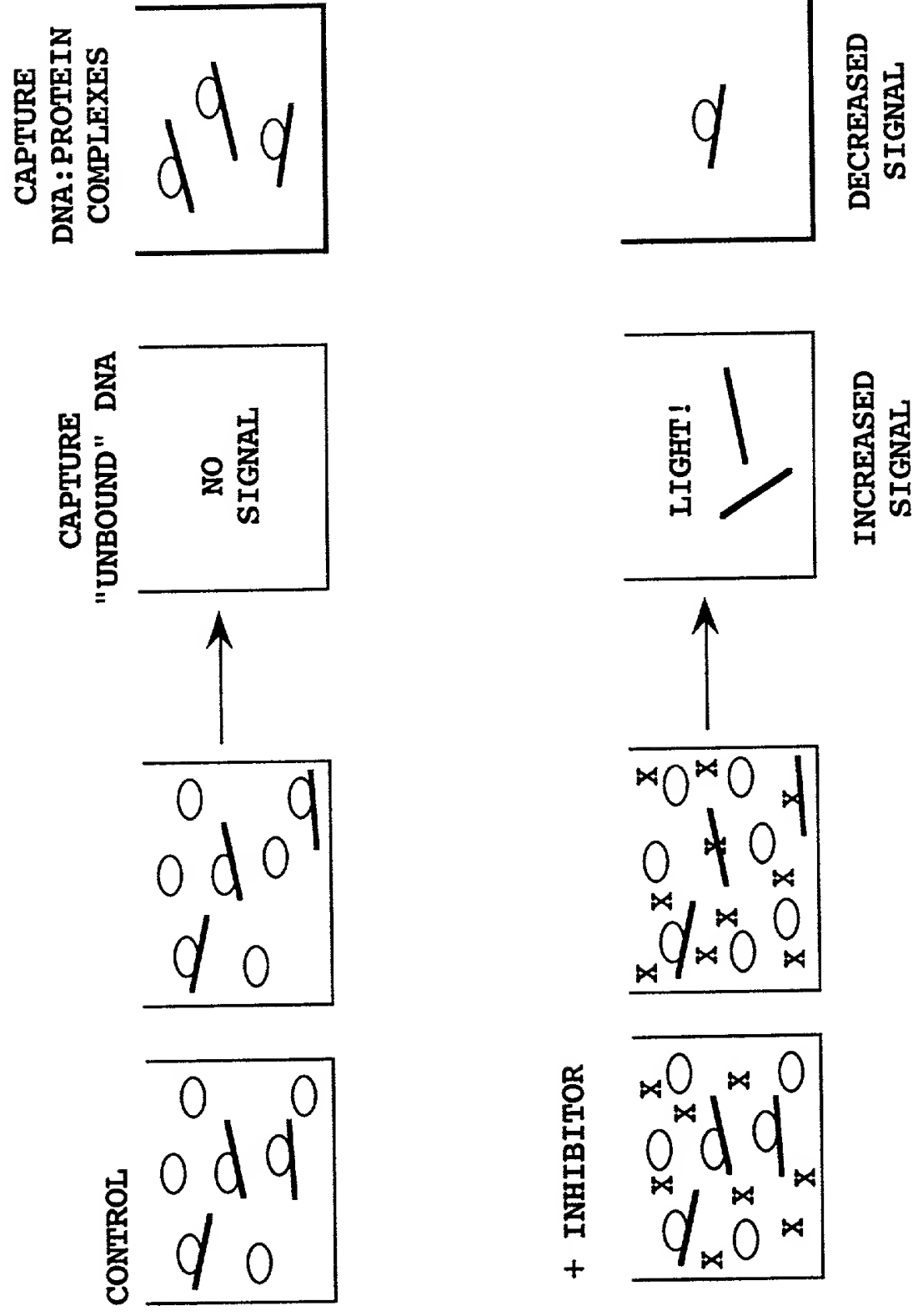


Fig. 2

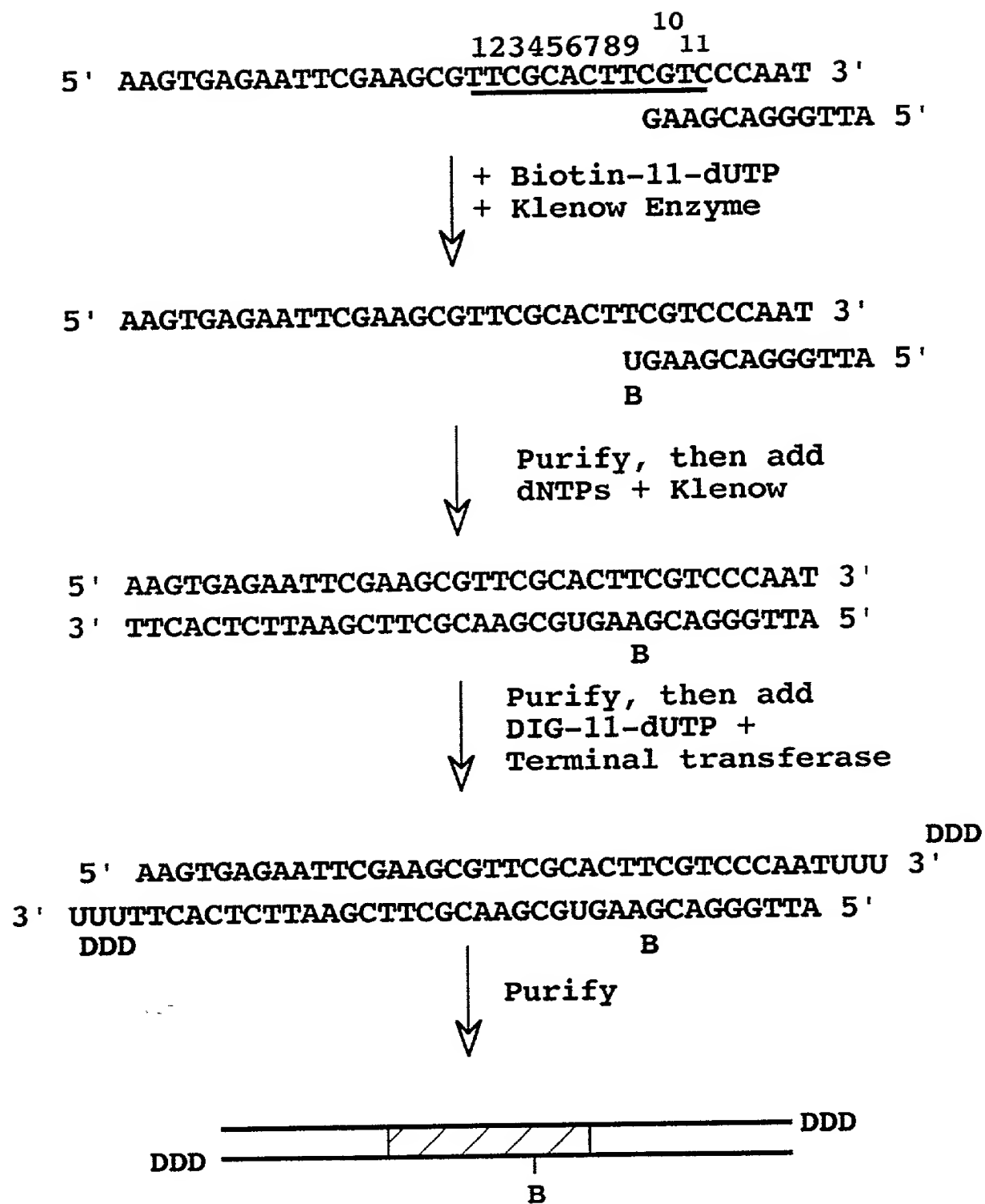


Fig. 4

	Test Sequence:	Screening Sequence:	Test Sequence:
UL9Z1	5' - <u>GCGCGCGCGCGTTCGCACTTCCGCCGCCGG</u> -3'		Z-DNA
UL9Z2	5' -GGCGCCGGCCGTTTCGCACTT <u>CGCGCGCGCG</u> -3'		Z-DNA
UL9 CCGG	5' -GGCCCGCCCCGTTTCGCACTTCCCGCCCCGG-3'		
UL9 GGGC	5' -GGCGGGCGCCGTTTCGCACTTGGGCGGGCGG-3'		
UL9 ATAT	5' -GGATATATACGTTTCGCACTTTAATTATTGG-3'		
UL9 polyA	5' -GGAAAAAACGTTTCGCACTTAAAAAAAGG-3'		
UL9 polyT	5' -GGTTTTTTTCGTTTCGCACTTTTTTTTTTGG-3'		
UL9 GCAC	5' -GGACGCACGCGTTTCGCACTTGCAGCAGCGG-3'		
ATori-1	5' -GCGTATATATCGTTTCGCACTTCGTCCCAAT-3'		
oriEco2	5' -GGCGAATTCGACGTTTCGCACTTCGTCCCAAT-3'		
oriEco3	5' -GGCGAATTCGATCGTTTCGCACTTCGTCCCAAT-3'		

Fig. 5

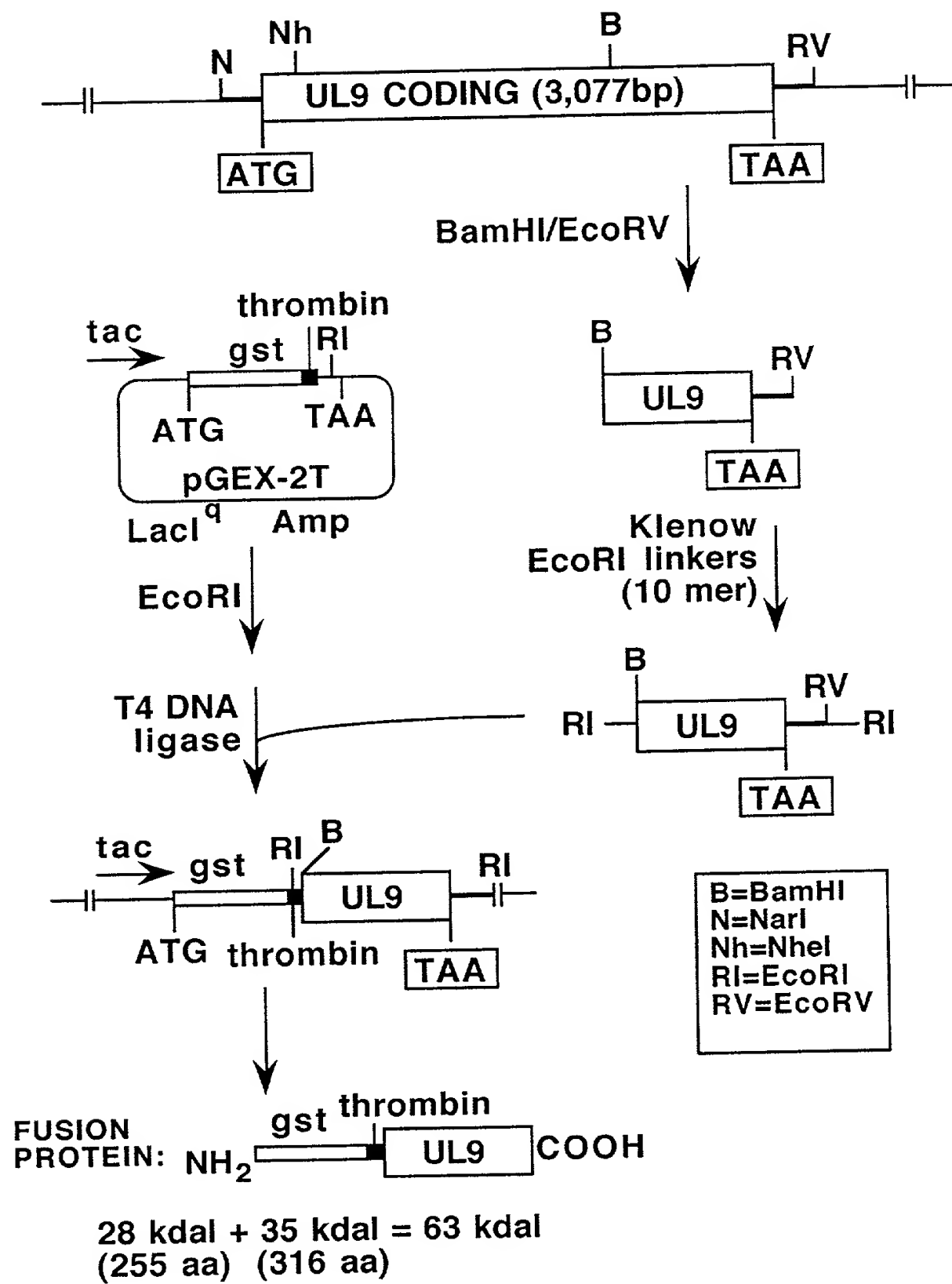


Fig. 6

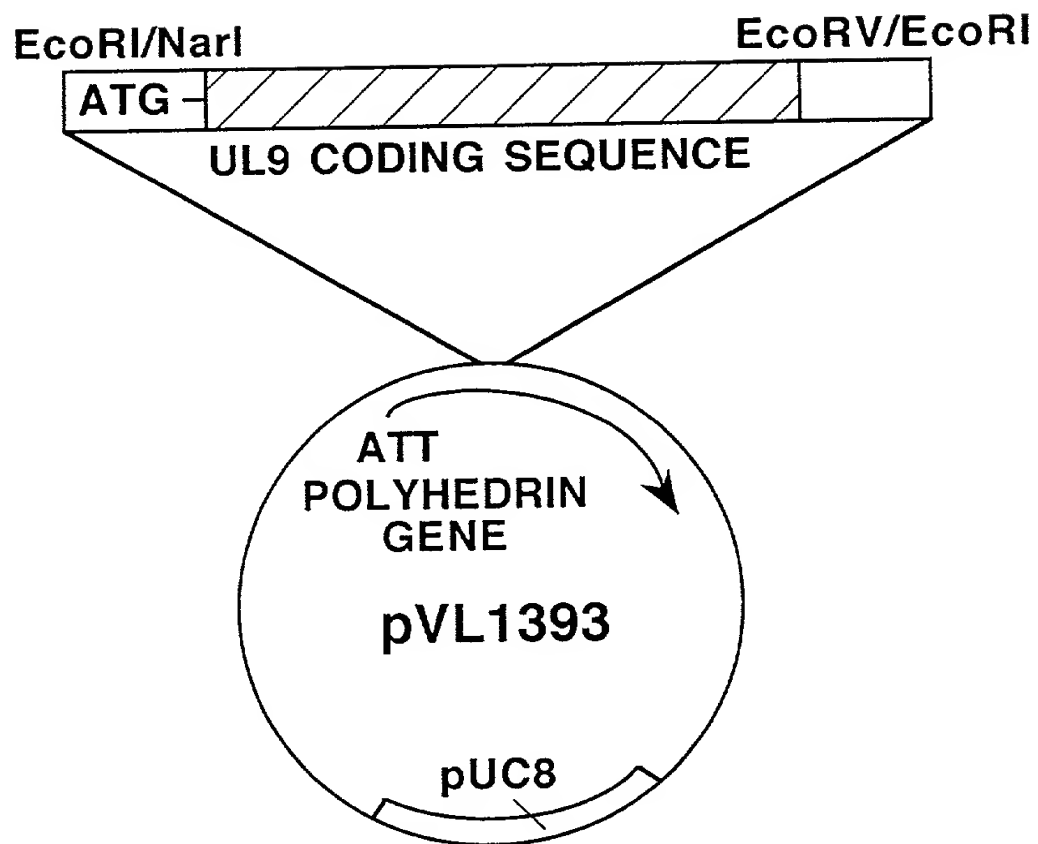


Fig. 7

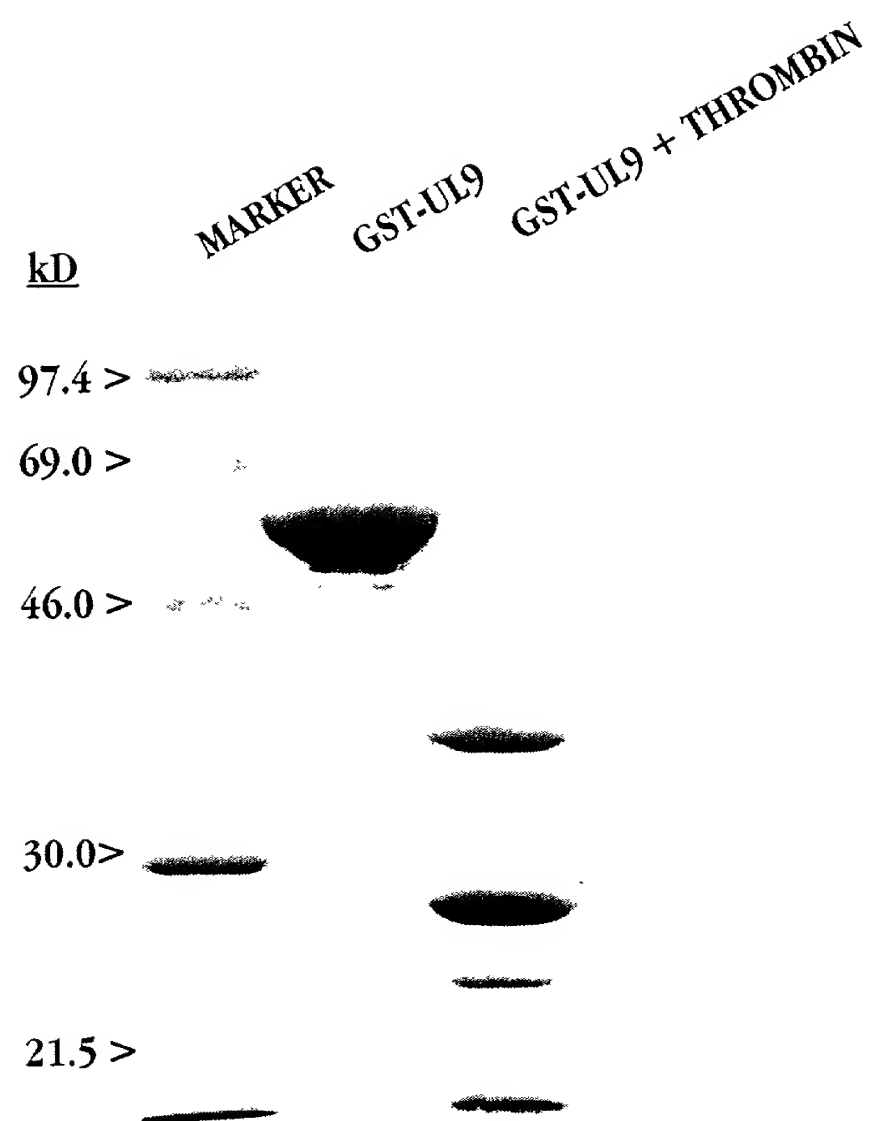


Fig. 8

0 5 10 15 20 60
UL9 CCCG
UL9 GGGC
oriECO2
ATori-1

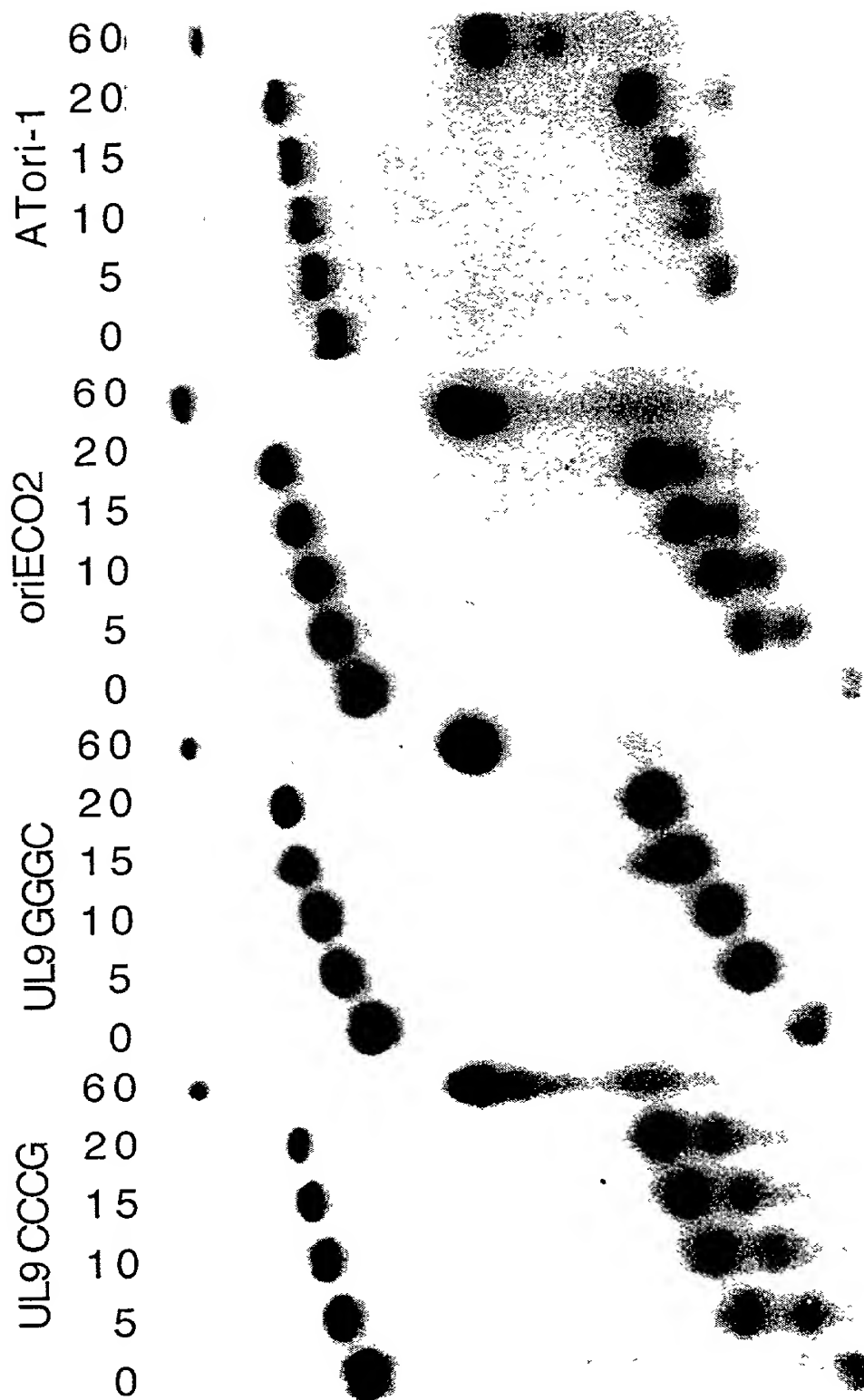


Fig. 9A

UL9 polyA
UL9 polyT
UL9 ATAT
oriECO3

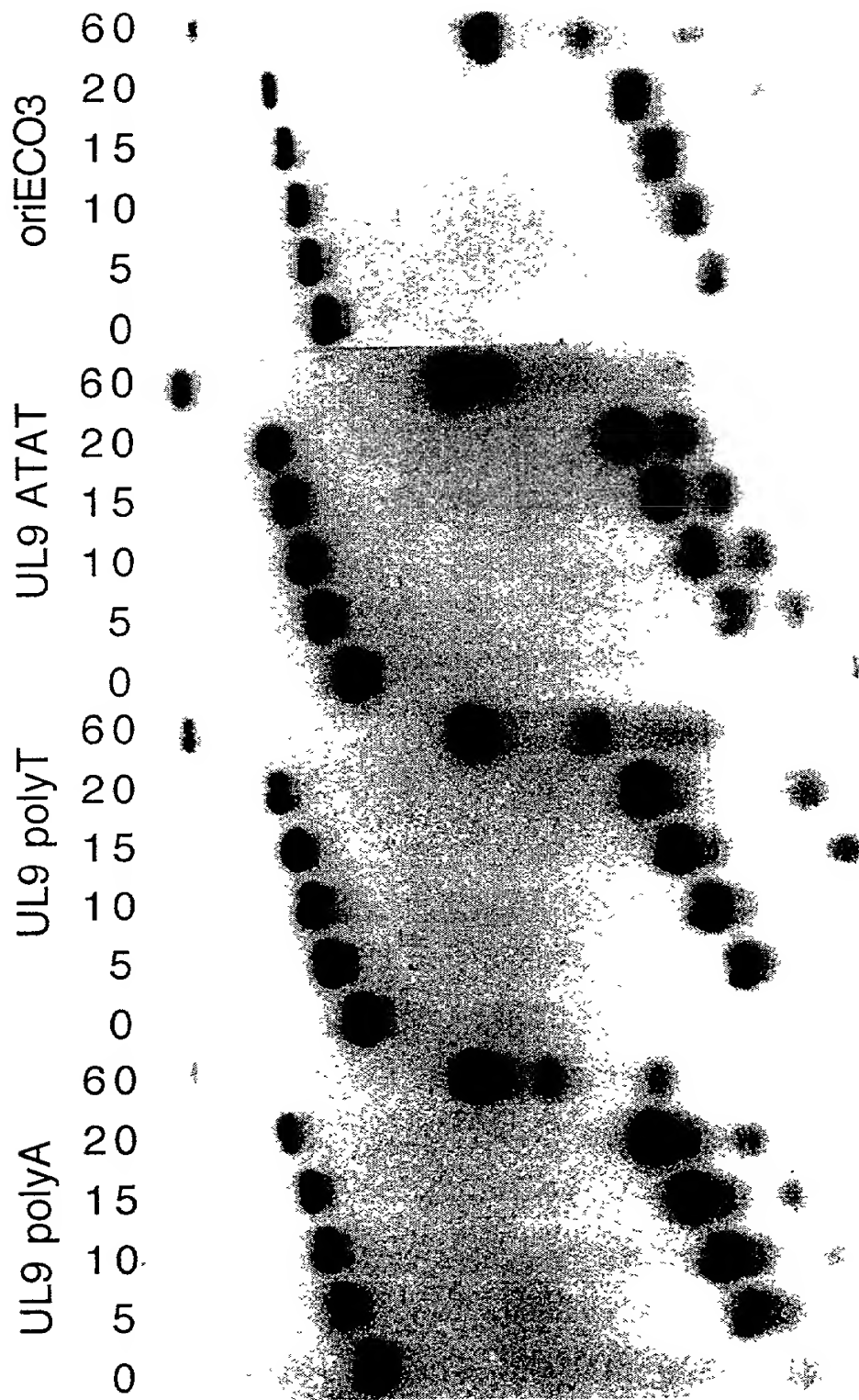


Fig. 9B

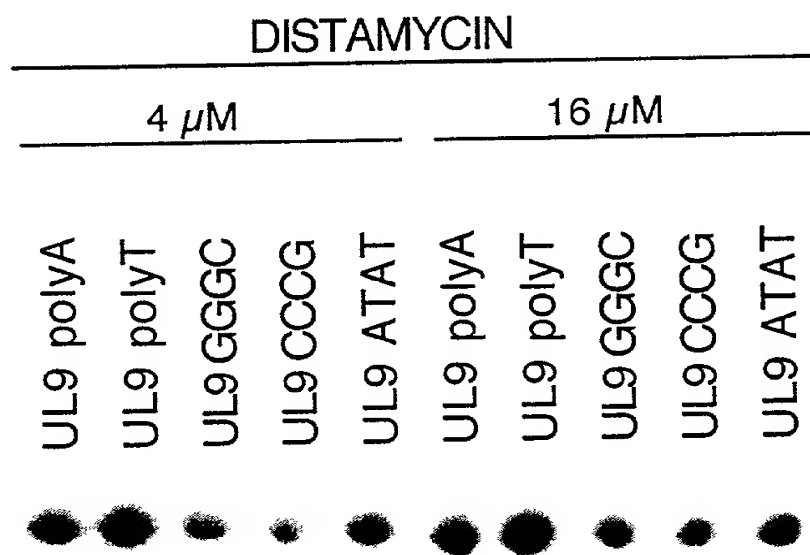
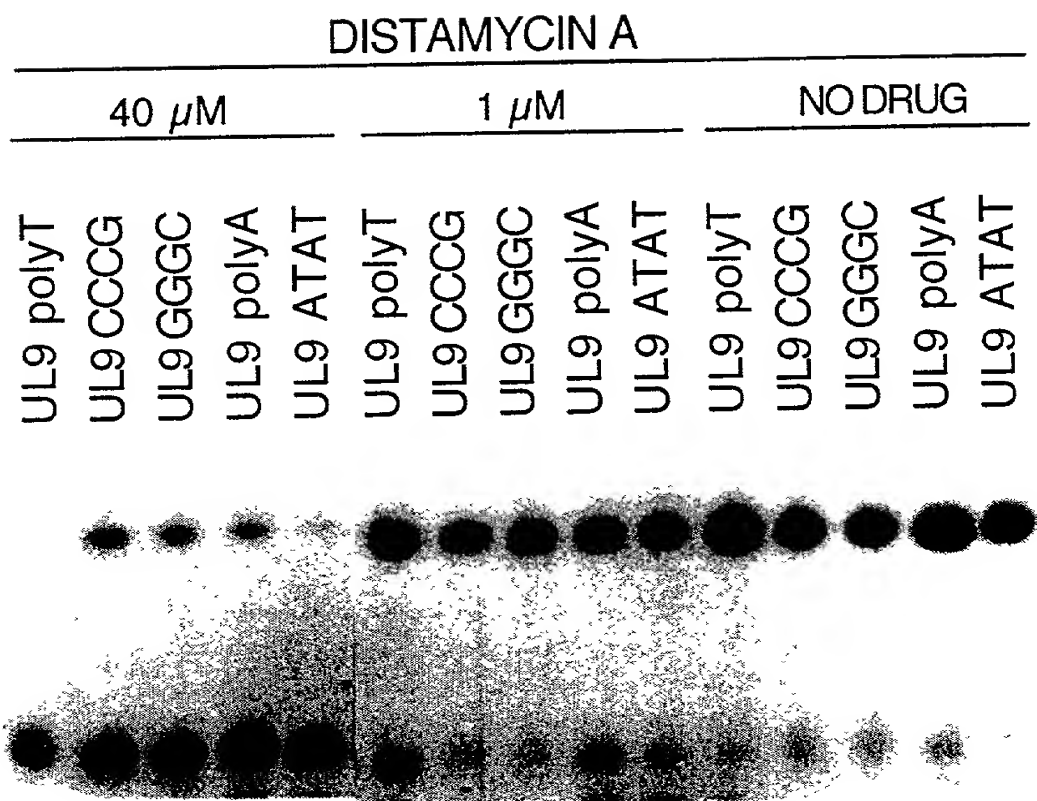


Fig. 10A

UL9 polyA
UL9 polyT
UL9 ATAT
UL9 CCCG
UL9 GGGC
oriECO2
oriECO3
ATori-1

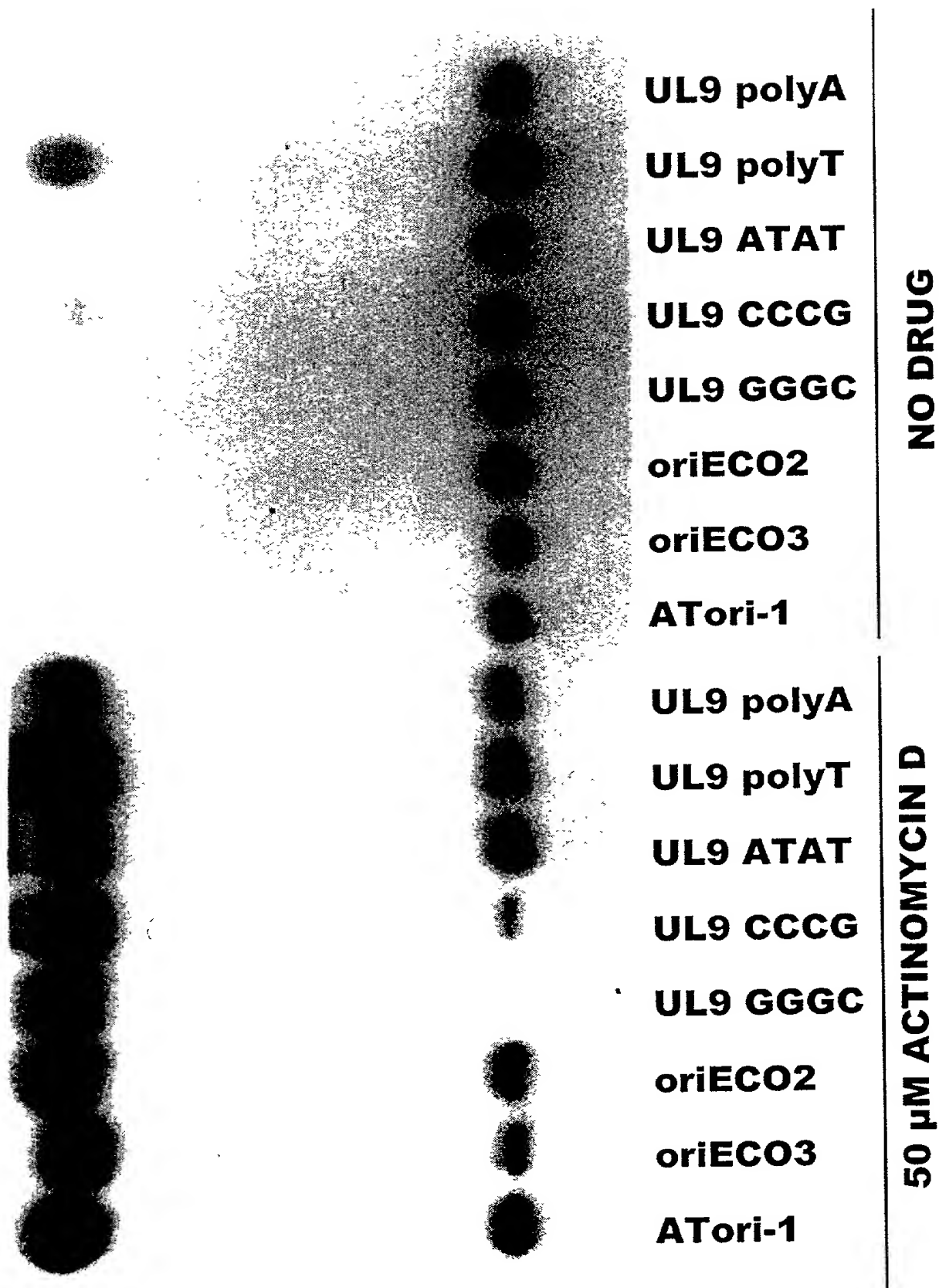


Fig. 10B

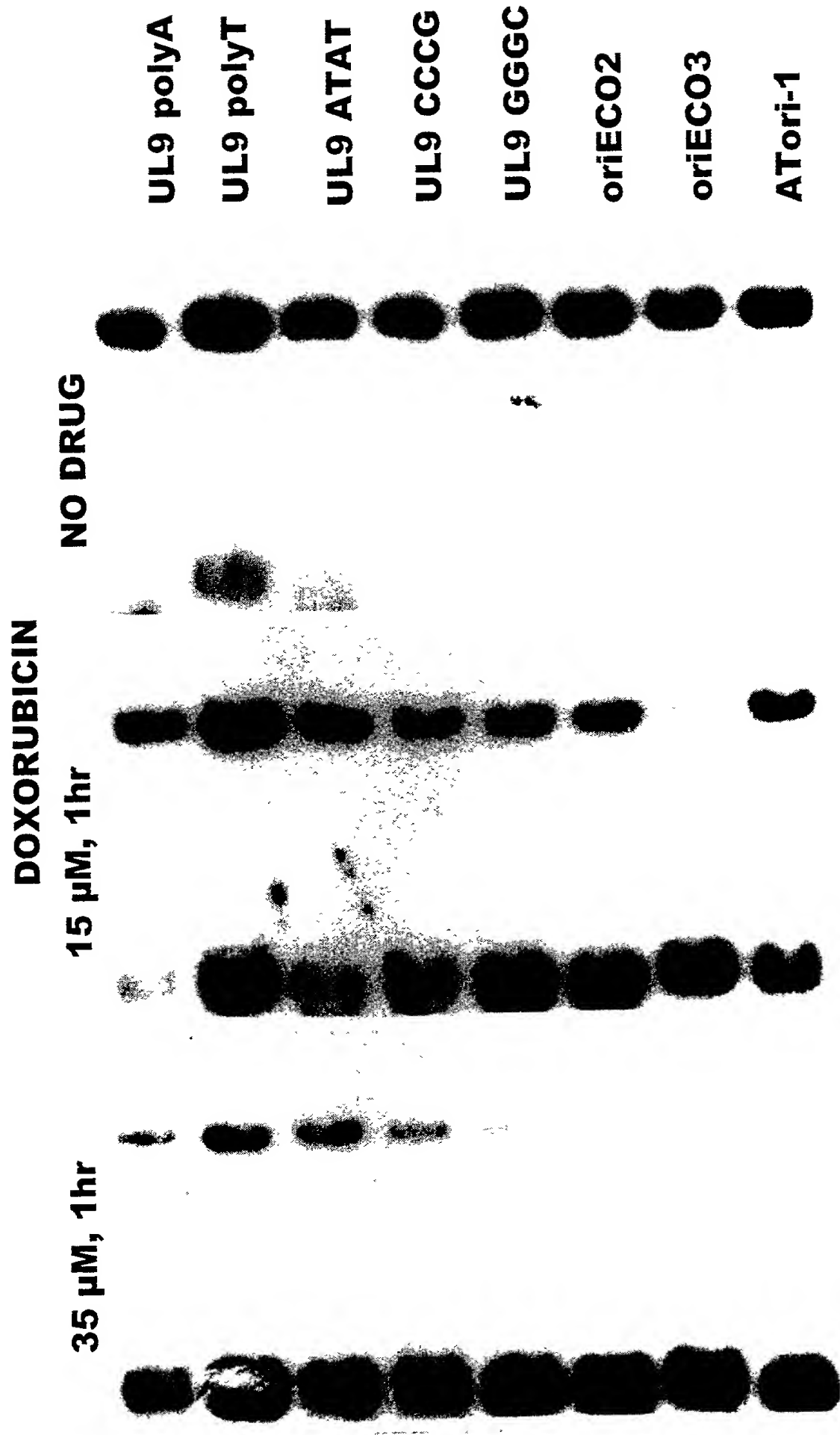


Fig. 10C

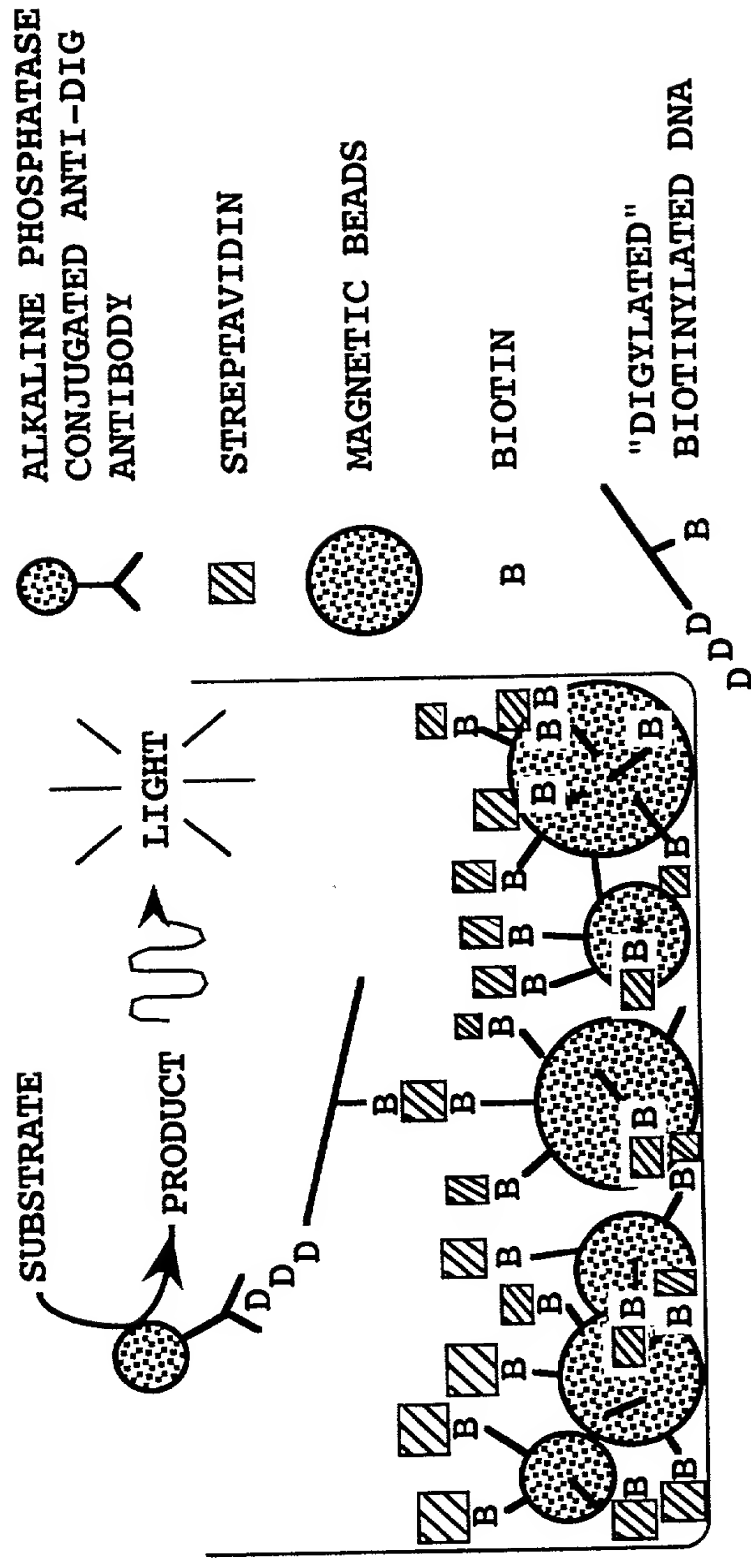


Fig. 11A

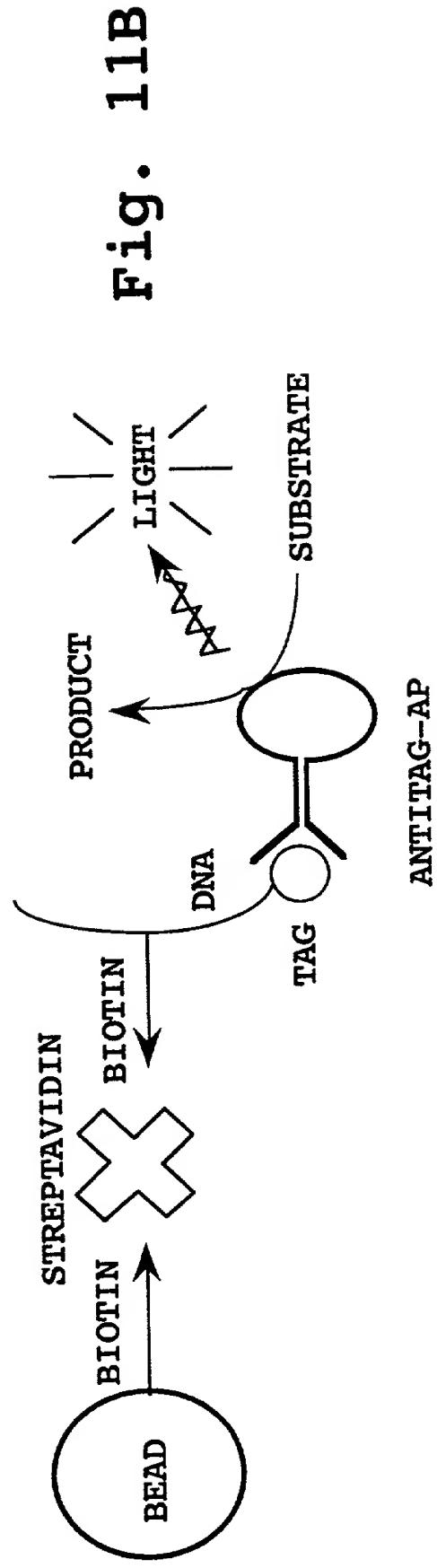


Fig. 11B

Test Mixtures

Sequence	<u>1</u>	<u>2</u>	<u>3</u>	<u>4</u>	<u>5</u>	<u>6</u>	<u>7</u>	<u>8</u>	<u>9</u>
<u>AGCTTTCGCACTTAGCT</u>	-	+	+	-	-	-	-	-	-
<u>AGCATTCGCACTTAGCA</u>	-	+	-	-	+	+	-	-	-
<u>AGCCTTCGCACTTAGCC</u>	-	+	-	-	-	-	-	-	+
<u>AGCGTTCGCACTTAGCG</u>	-	+	-	-	-	-	-	+	-
<u>TGCTTTCGCACTTTGCT</u>	-	+	-	-	-	+	-	+	-
<u>TGCAATTCGCACTTTGCA</u>	-	+	-	-	+	-	-	+	+
<u>TGCCCTTCGCACTTTGCC</u>	-	+	-	-	-	-	-	+	+
<u>TGCGTTCGCACTTTGCG</u>	-	+	-	-	-	-	-	+	-
;	:	:	:	:	:	:	:	:	:
;	:	:	:	:	:	:	:	:	:
<u>CCATTTCGCACTTCCAT</u>	-	+	-	-	+	-	-	-	+
<u>CCCTTTCGCACTTCCCT</u>	-	+	-	-	-	-	-	+	+
<u>CCGTTTCGCACTTCCGT</u>	-	+	-	-	-	-	-	-	+
<u>CCTTTTCGCACTTCCTT</u>	-	+	-	-	-	-	-	+	+
;	:	:	:	:	:	:	:	:	:

Fig. 12

SEQUENCE

AAAA	001	ATCG	055	CGTA	109
AAAC	002	ATCT	056	CGTC	110
AAAG	003	ATGA	057	CGTG	111
AAAT	004	ATGC	058	CGTT	112
AACA	005	ATGG	059	CTAA	113
AACC	006	ATGT	060	CTAC	114
AACG	007	ATTA	061	CTAG	115
AACT	008	ATTC	062	CTAT	116
AAGA	009	ATTG	063	CTCA	117
AAGC	010	ATTT	064	CTCC	118
AAGG	011	CAAA	065	CTCG	119
AAGT	012	CAAC	066	CTCT	120
AATA	013	CAAG	067	CTGA	121
AATC	014	CAAT	068	CTGC	122
AATG	015	CACA	069	CTGG	123
AATT	016	CACC	070	CTGT	124
ACAA	017	CACG	071	CTTA	125
ACAC	018	CACT	072	CTTC	126
ACAG	019	CAGA	073	CTTG	127
ACAT	020	CAGC	074	CTTT	128
ACCA	021	CAGG	075	GAAA	129
ACCC	022	CAGT	076	GAAC	130
ACCG	023	CATA	077	GAAG	131
ACCT	024	CATC	078	GAAT	132
ACGA	025	CATG	079	GACA	133
ACGC	026	CATT	080	GACC	134
ACGG	027	CCAA	081	GACG	135
ACGT	028	CCAC	082	GACT	136
ACTA	029	CCAG	083	GAGA	137
ACTC	030	CCAT	084	GAGC	138
ACTG	031	CCCA	085	GAGG	139
ACTT	032	CCCC	086	GAGT	140
AGAA	033	CCCG	087	GATA	141
AGAC	034	CCCT	088	GATC	142
AGAG	035	CCGA	089	GATG	143
AGAT	036	CCGC	090	GATT	144
AGCA	037	CCGG	091	GCAA	145
AGCC	038	CCGT	092	GCAC	146
AGCG	039	CCTA	093	GCAG	147
AGCT	040	CCTC	094	GCAT	148
AGGA	041	CCTG	095	GCCA	149
AGGC	042	CCTT	096	GCCC	150
AGGG	043	CGAA	097	GCCG	151
AGGT	044	CGAC	098	GCCT	153
AGTA	045	CGAG	099	GCGC	154
AGTC	046	CGAT	100	GCGG	155
AGTG	047	CGCA	101	GCGT	156
AGTT	048	CGCC	102	GCTA	157
ATAA	049	CGCG	103	GCTC	158
ATAC	050	CGCT	104	GCTG	159
ATAG	051	CGGA	105	GCTT	160
ATAT	052	CGGC	106	GGAA	161
ATCA	053	CGGG	107	GGAC	162
ATCC	054	CGGT	108	GGAG	163

Fig. 13A

GGAT	164	TCGC	218
GGCA	165	TCGG	219
GGCC	166	TCGT	220
GGCG	167	TCTA	221
GGCT	168	TCTC	222
GGGA	169	TCTG	223
GGGC	170	TCTT	224
GGGG	171	TGAA	225
GGGT	172	TGAC	226
GGTA	173	TGAG	227
GGTC	174	TGAT	228
GGTG	175	TGCA	229
GGTT	176	TGCC	230
GTAA	177	TGCG	231
GTAC	178	TGCT	232
GTAG	179	TGGA	233
GTAT	180	TGGC	234
GTCA	181	TGGG	235
GTCC	182	TGGT	236
GTCG	183	TGTA	237
GTCT	184	TGTC	238
GTGA	185	TGTG	239
GTGC	186	TGTT	240
GTGG	187	TTAA	241
GTGT	188	TTAC	242
GTTA	189	TTAG	243
G TTC	190	TTAT	244
GTTG	191	TTCA	245
GTTT	192	TTCC	246
TAAA	193	TTCG	247
TAAC	194	TTCT	248
TAAG	195	TTGA	249
TAAT	196	TTGC	250
TACA	197	TTGG	251
TACC	198	TTGT	252
TACG	199	TTTA	253
TACT	200	TTTC	254
TAGA	201	TTTG	255
TAGC	202	TTTT	256
TAGG	203		
TAGT	204		
TATA	205		
TATC	206		
TATG	207		
TATT	208		
TCAA	209		
TCAC	210		
TCAG	211		
TCAT	212		
TCCA	213		
TCCC	214		
TCCG	215		
TCCT	216		
TCGA	217		

Fig. 13B

GATC	AGTC	TAGC	CGAT
GACT	AGCT	TACG	CGTA
GTCA	ATCG	TGCA	CATG
GTAC	ATGC	TGAC	CAGT
GCTA	ACTG	TCAG	CTAG
GCAT	ACGT	TCGA	CTGA

Fig. 14A

Screening Sequence	
GCGTANXXXX	<u>CGTTCGCACTT</u> XXXXCTTCGTCCCAAT
CGCATN <u>YYYY</u>	GCAAGCGTGA <u>YYYY</u> GAAGCAGGGTTA
Test Site	Test Site

Fig. 14B

Sort by average rank:												
rank	oligo	sequence	%r918	rank	%r918	rank	%r1022	rank	%r1022	rank	ave. %r	ave rank
1	246	TTCC	47	14	44	14	41	4	27	3	40	9
2	242	TTAC	49	19	47	19	55	17	46	15	49	18
3	198	TACC	57	43	48	22	50	7	39	10	48	21
4	206	TATC	50	20	46	18	54	16	59	45	52	25
5	7	AACG	56	38	56	52	48	6	34	4	49	25
6	247	TTCG	56	36	49	26	58	20	54	34	54	29
7	254	TTTC	51	21	35	4	66	46	63	59	54	33
8	27	ACGG	55	30	55	49	63	33	51	24	56	34
9	202	TAGC	65	74	46	16	67	52	18	1	49	36
10	243	TTAG	61	57	53	43	58	21	51	23	56	36
11	251	TTGG	61	59	44	13	60	23	62	53	57	37
12	194	TAAC	66	83	51	35	45	5	52	30	54	38
13	3	AAAG	60	54	58	60	65	37	42	12	56	41
14	6	AACC	70	101	56	51	51	9	34	5	53	42
15	199	TACG	66	82	53	45	51	8	53	31	56	42
16	66	CAAC	54	27	58	59	70	64	52	29	59	45
17	34	AGAC	55	32	52	41	63	32	67	75	59	45
18	2	AAAC	72	117	50	31	52	12	51	25	56	46
19	54	ATCC	55	29	58	61	75	93	36	7	56	48
20	11	AAGG	68	90	59	62	60	26	48	18	59	49
21	39	AGCG	49	18	53	44	80	138	39	8	55	52
22	38	AGCC	55	34	46	17	80	133	58	41	60	56
23	195	TAAG	70	105	63	72	57	19	54	32	61	57
24	248	TTCT	70	104	52	40	65	38	60	46	61	57
25	26	ACGC	58	45	49	25	78	116	59	44	61	58
26	22	ACCC	64	72	49	28	65	40	71	93	62	58
27	58	ATGC	63	67	65	77	68	53	55	37	63	59
28	43	AGGG	41	6	51	38	86	170	49	21	57	59
29	214	TCCC	68	87	62	70	65	41	58	42	63	60
30	42	AGGC	43	8	49	24	90	195	44	14	56	60
31	207	TATG	58	46	67	87	62	29	68	79	64	60
32	23	ACCG	54	25	58	57	80	134	52	26	61	61
33	51	ATAG	48	15	73	111	68	55	63	63	63	61
34	219	TCGG	62	60	74	114	65	36	61	48	65	65
35	46	AGTC	18	2	42	9	74	90	80	160	54	65
36	249	TTGA	71	109	51	36	71	71	62	55	64	68
37	250	TTGC	56	35	50	30	67	49	80	161	63	69
38	119	CTCG	54	26	85	176	61	27	60	47	65	69
39	55	ATCG	56	37	84	169	66	44	52	28	64	70
40	215	TCCG	62	61	58	55	73	81	70	86	66	71
41	231	TGCG	63	66	65	79	70	63	69	83	67	73
42	161	GGAA	43	10	72	107	79	128	67	73	65	80
43	255	TTTG	59	48	51	37	64	35	87	199	65	80
44	14	AATC	71	112	50	33	82	152	52	27	64	81

Fig. 15A

45	238	TGTC	72	119	64	74	65	42	70	89	68	81
46	35	AGAG	56	41	55	47	87	184	62	54	65	82
47	241	TTAA	76	137	84	170	51	10	41	11	63	82
48	18	ACAC	66	80	50	29	97	216	36	6	62	83
49	47	AGTG	51	22	42	10	105	231	65	68	66	83
50	245	TTCA	81	157	66	84	60	25	65	69	68	84
51	205	TATA	70	102	66	85	71	70	69	82	69	85
52	210	TCAC	65	75	45	15	21	2	*57.3	250	43	86
53	36	AGAT	70	100	43	11	102	224	39	9	64	86
54	244	TTAT	80	149	62	69	61	28	71	99	69	86
55	234	TGGC	56	40	61	68	82	150	70	88	67	87
56	256	TTTT	54	28	58	58	71	67	86	195	67	87
57	193	TAAA	74	124	74	117	68	54	63	61	70	89
58	203	TAGG	84	178	59	63	62	30	70	90	69	90
59	63	ATTG	60	51	76	122	80	137	63	56	70	92
60	227	TGAG	75	126	39	6	71	73	81	164	67	92
61	116	CTAT	73	121	74	118	65	43	70	87	71	92
62	217	TCGA	60	53	85	175	69	59	71	95	72	96
63	59	ATGG	62	65	82	150	79	130	56	39	70	96
64	62	ATTC	64	69	71	102	93	203	43	13	68	97
65	185	GTGA	44	12	62	71	76	105	87	201	67	97
66	61	ATTA	77	140	87	179	67	50	49	22	70	98
67	50	ATAC	54	24	71	97	105	232	56	38	71	98
68	235	TGGG	60	52	71	104	78	115	76	121	71	98
69	166	GGCC	80	148	24	1	77	114	77	133	65	99
70	107	CGGG	65	78	100	218	67	51	61	50	73	99
71	232	TGCT	69	97	49	27	73	79	87	198	70	100
72	158	GCTC	33	3	66	83	71	72	131	243	75	100
73	19	ACAG	69	95	65	75	91	197	54	36	70	101
74	10	AAGC	80	151	70	93	73	82	70	85	73	103
75	208	TATT	70	106	72	105	75	97	73	105	72	103
76	1	AAAA	83	171	79	137	67	47	63	58	73	103
77	182	GTCC	76	135	60	66	70	65	79	150	71	104
78	157	GCTA	49	16	97	209	77	111	68	81	73	104
79	191	GTTG	110	244	43	12	76	102	63	60	73	105
80	172	GGGT	39	4	58	56	89	192	81	168	67	105
81	150	GCCC	58	44	80	142	86	172	63	62	72	105
82	15	AATG	68	88	70	94	108	237	22	2	67	105
83	196	TAAT	94	220	67	86	66	45	67	74	74	106
84	187	GTGG	44	11	100	220	69	58	78	140	73	107
85	184	GTCT	62	62	48	23	77	109	100	236	72	108
86	115	CTAG	70	98	94	203	60	24	73	106	74	108
87	120	CTCT	61	56	114	246	59	22	73	107	77	108
88	167	GGCG	65	73	81	145	80	135	68	80	73	108
89	239	TGTG	72	114	37	5	81	144	82	171	68	109
90	233	TGGA	66	84	65	78	76	106	82	170	72	110

Fig. 15B

91	52	ATAT	64	70	94	199	78	123	61	49	74	110
92	220	TCGT	73	122	47	21	83	157	78	142	70	111
93	183	GTCG	66	81	83	158	69	57	79	146	74	111
94	25	ACGA	60	55	74	116	100	221	62	52	74	111
95	226	TGAC	71	111	73	110	71	69	80	156	74	112
96	33	AGAA	55	33	82	155	122	246	48	16	77	113
97	114	CTAC	61	58	77	125	54	15	*78.17	253	84	113
98	211	TCAG	75	130	70	95	75	100	76	126	74	113
99	104	CGCT	69	93	92	194	64	34	77	131	75	113
100	142	GATC	64	68	33	3	84	160	92	224	68	114
101	230	TGCC	73	123	60	67	73	77	85	188	73	114
102	209	TCAA	72	115	69	91	84	158	71	92	74	114
103	162	GGAC	41	7	83	157	67	48	149	244	85	114
104	67	CAAG	86	184	66	82	86	174	49	19	72	115
105	252	TTGT	82	162	56	50	77	113	78	136	73	115
106	222	TCTC	69	94	77	127	84	163	68	77	75	115
107	174	GGTC	65	76	107	237	54	14	77	134	76	115
108	30	ACTC	73	120	65	81	131	250	48	17	79	117
109	71	CACG	13	1	83	162	88	186	76	122	65	118
110	45	AGTA	60	50	77	126	106	234	64	66	77	119
111	201	TAGA	94	216	77	129	72	75	63	57	76	119
112	29	ACTA	81	153	42	8	131	249	64	67	79	119
113	24	ACCT	56	39	93	195	95	210	54	35	75	120
114	31	ACTG	68	89	73	109	112	240	58	43	78	120
115	175	GGTG	71	110	94	200	55	18	80	158	75	122
116	131	GAAG	69	91	71	100	78	120	83	175	75	122
117	229	TGCA	76	136	83	163	78	118	67	72	76	122
118	163	GGAG	49	17	106	234	69	60	85	184	77	124
119	90	CCGC	83	172	82	148	69	56	75	119	77	124
120	253	TTTA	75	128	72	106	74	85	84	180	76	125
121	118	CTCC	78	142	57	54	75	98	89	207	75	125
122	151	GCCG	52	23	110	243	84	164	67	71	78	125
123	155	GCGG	62	64	69	92	108	236	75	114	79	127
124	221	TCTA	75	134	71	98	82	153	77	129	76	129
125	179	GTAG	141	250	59	64	75	95	73	108	87	129
126	122	CTGC	89	200	76	121	74	91	74	109	78	130
127	197	TACA	87	192	88	183	71	68	68	78	79	130
128	143	GATG	62	63	57	53	105	229	84	181	77	132
129	170	GGGC	43	9	92	190	78	119	89	209	75	132
130	44	AGGT	65	77	69	90	124	247	75	116	83	133
131	57	ATGA	72	118	88	181	92	201	57	40	77	135
132	13	AATA	86	186	106	235	14	1	76	120	70	136
133	130	GAAC	90	205	65	76	80	136	76	125	78	136
134	236	TGGT	75	132	60	65	78	122	92	225	76	136
135	216	TCCT	83	169	71	99	82	149	77	130	78	137
136	41	AGGA	81	158	51	39	151	253	71	97	89	137

Fig. 15C

137	237	TGTA	82	166	74	115	74	89	83	178	78	137
138	9	AAGA	87	191	78	133	82	154	67	70	79	137
139	218	TCGC	72	113	78	132	75	96	90	211	79	138
140	56	ATCT	75	133	81	146	89	189	69	84	79	138
141	108	CGGT	64	71	94	201	73	78	88	205	80	139
142	98	CGAC	94	219	84	168	54	13	80	159	78	140
143	145	GCAA	57	42	105	230	77	112	84	179	81	141
144	112	CGTT	80	152	82	151	76	101	81	165	80	142
145	96	CCTT	69	92	29	2	106	235	105	241	77	143
146	48	AGTT	70	107	47	20	116	243	87	200	80	143
147	171	GGGG	55	31	112	244	77	107	86	194	82	144
148	12	AAGT	76	138	89	184	102	223	54	33	80	145
149	154	GCGC	89	203	74	113	96	214	62	51	80	145
150	89	CCGA	95	222	50	32	74	88	104	239	81	145
151	240	TGTT	79	146	65	80	86	173	84	183	79	146
152	79	CATG	92	209	79	136	78	121	75	118	81	146
153	165	GGCA	60	49	105	232	72	74	95	231	83	147
154	204	TAGT	96	225	86	178	77	108	68	76	81	147
155	87	CCCG	85	182	82	152	73	80	83	174	81	147
156	200	TACT	97	230	84	167	74	86	74	110	82	148
157	132	GAAT	75	129	106	236	70	61	81	167	83	148
158	146	GCAC	59	47	115	248	87	183	75	115	84	148
159	49	ATAA	65	79	84	166	128	248	72	102	87	149
160	4	AAAT	86	183	105	231	78	117	64	65	83	149
161	70	CACC	89	199	96	207	75	99	71	98	83	151
162	110	CGTC	98	233	92	191	73	83	71	96	83	151
163	28	ACGT	83	168	55	48	146	252	78	138	90	152
164	8	AACT	81	160	83	159	84	162	77	128	81	152
165	92	CCGT	81	159	77	130	73	84	102	238	84	153
166	5	AACA	83	170	93	197	84	161	71	91	83	155
167	84	CCAT	108	242	54	46	87	177	80	155	82	155
168	190	GTTC	84	174	68	88	85	168	85	192	80	156
169	160	GCTT	44	13	89	186	92	202	92	222	79	156
170	78	CATC	92	213	83	161	79	126	76	124	83	156
171	123	CTGG	86	185	89	185	81	145	74	111	83	157
172	228	TGAT	102	240	71	101	81	146	78	143	83	158
173	135	GACG	82	164	79	135	89	191	79	147	82	159
174	149	GCCA	70	99	97	210	105	228	72	101	86	160
175	128	CTTT	79	144	77	128	85	169	88	203	82	161
176	159	GCTG	40	5	104	229	86	171	105	240	84	161
177	17	ACAA	82	167	112	245	96	213	49	20	85	161
178	225	TGAA	91	206	76	124	81	140	83	176	83	162
179	164	GGAT	67	86	100	221	82	148	85	191	84	162
180	178	GTAC	92	212	75	120	85	166	79	149	83	162
181	77	CATA	155	252	50	34	102	222	78	139	96	162
182	105	CGGA	84	173	110	242	52	11	92	223	84	162

Fig. 15D

183	53	ATCA	75	131	83	156	105	230	77	135	85	163
184	40	AGCT	75	127	71	103	104	226	87	197	84	163
185	173	GGTA	71	108	96	206	88	187	80	154	83	164
186	156	GCGT	74	125	76	123	119	245	81	162	88	164
187	88	CCCT	88	193	80	138	74	92	101	237	86	165
188	32	ACTT	69	96	82	154	134	251	81	166	92	167
189	144	GATT	67	85	80	143	100	220	91	220	85	167
190	223	TCTG	77	139	95	204	77	110	91	217	85	168
191	134	GACC	97	229	69	89	87	180	82	173	84	168
192	75	CAGG	96	228	73	108	87	182	79	153	84	168
193	91	CCGG	80	150	81	147	81	141	97	233	85	168
194	72	CACT	93	215	107	238	83	156	63	64	87	168
195	153	GCGA	72	116	100	219	111	239	72	103	89	169
196	192	GTTT	125	248	74	119	84	159	79	151	91	169
197	137	GAGA	89	201	40	7	103	225	*248.59	248	78	170
198	127	CTTG	81	156	92	193	82	151	85	185	85	171
199	93	CCTA	86	187	92	192	76	103	88	204	86	172
200	176	GGTT	117	246	70	96	81	142	88	202	89	172
201	213	TCCA	77	141	78	134	87	178	99	234	85	172
202	60	ATGT	79	145	83	160	116	242	78	141	89	172
203	125	CTTA	86	189	52	42	95	211	*79.5	254	78	174
204	168	GGCT	101	239	85	172	79	129	80	157	86	174
205	139	GAGG	92	210	94	198	85	167	76	123	87	175
206	147	GCAG	70	103	120	251	90	196	79	152	90	176
207	37	AGCA	79	143	81	144	94	207	89	210	86	176
208	101	CGCA	79	147	88	182	78	124	*65.76	252	82	176
209	224	TCTT	93	214	73	112	84	165	91	216	85	177
210	103	CGCG	91	207	116	250	62	31	91	219	90	177
211	180	GTAT	179	254	100	216	75	94	79	144	108	177
212	64	ATTT	84	175	83	165	94	208	82	172	86	180
213	141	GATA	95	224	82	153	91	200	79	145	87	181
214	140	GAGT	117	245	63	73	96	215	85	189	90	181
215	169	GGGA	82	165	145	254	89	190	75	113	98	181
216	97	CGAA	153	251	101	223	24	3	798	246	269	181
217	94	CCTC	92	211	82	149	86	175	85	190	86	181
218	186	GTGC	205	255	356	256	74	87	77	127	178	181
219	82	CCAC	97	232	85	174	80	131	86	193	87	183
220	113	CTAA	85	180	109	240	70	62	*60.31	251	88	183
221	212	TCAT	89	198	77	131	89	193	91	215	87	184
222	65	CAAA	84	179	116	249	95	209	72	100	92	184
223	99	CGAG	103	241	99	215	65	39	180	245	112	185
224	102	CGCC	88	195	106	233	70	66	*35.62	249	88	186
225	76	CAGT	96	227	85	177	93	205	78	137	88	187
226	126	CTTC	81	161	90	187	81	147	*88.2	256	84	188
227	21	ACCA	85	181	99	213	113	241	75	117	93	188
228	189	GTTA	178	253	210	255	81	143	72	104	135	189

Fig. 15E

229	69	CACA	82	163	83	164	98	219	90	212	88	190
230	111	CGTG	81	155	109	239	81	139	93	227	91	190
231	138	GAGC	84	176	80	139	91	199	*171.29	247	85	190
232	100	CGAT	89	202	80	141	163	255	81	163	103	190
233	74	CAGC	95	223	94	202	78	125	90	213	89	191
234	106	CGGC	99	236	98	211	93	204	75	112	91	191
235	129	GAAA	87	190	93	196	87	185	87	196	89	192
236	181	GTCA	98	234	98	212	76	104	91	218	91	192
237	73	CAGA	97	231	102	226	98	217	71	94	92	192
238	20	ACAT	89	196	91	188	109	238	79	148	92	193
239	83	CCAG	90	204	85	171	96	212	85	186	89	193
240	152	GCCT	88	194	91	189	94	206	85	187	89	194
241	95	CCTG	89	197	85	173	87	179	99	235	90	196
242	148	GCAT	94	218	100	217	98	218	77	132	92	196
243	81	CCAA	91	208	101	224	88	188	83	177	91	199
244	177	GTAA	130	249	133	252	79	127	81	169	106	199
245	117	CTCA	81	154	101	222	89	194	95	230	91	200
246	109	CGTA	120	247	115	247	72	76	97	232	101	201
247	121	CTGA	101	238	95	205	87	181	84	182	92	202
248	16	AATT	96	226	80	140	117	244	89	206	95	204
249	86	CCCC	84	177	103	228	91	198	93	226	93	207
250	85	CCCA	99	237	102	225	83	155	115	242	100	215
251	188	GTGT	217	256	136	253	80	132	92	221	131	216
252	124	CTGT	94	221	96	208	106	233	89	208	96	218
253	133	GACA	108	243	110	241	87	176	90	214	99	219
254	136	GACT	86	188	103	227	159	254	93	228	110	224
255	68	CAAT	99	235	99	214	105	227	94	229	99	226
256	80	CATT	94	217	87	180	348	256	*838.83	255	176	227

Fig. 15F

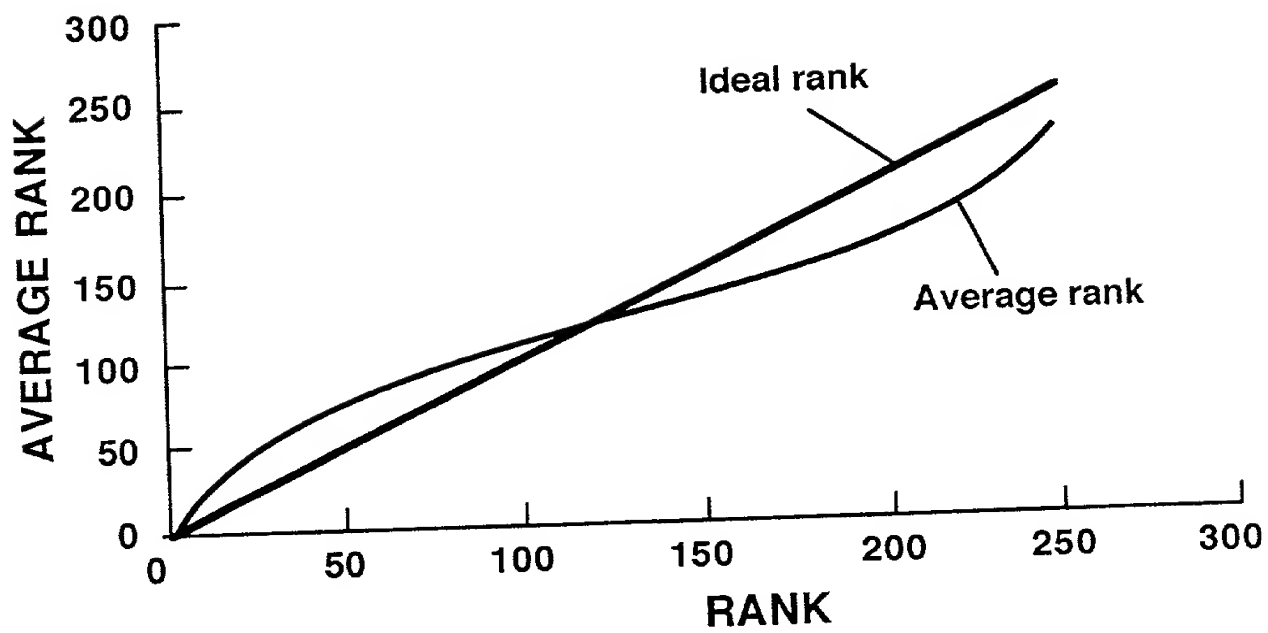


Fig. 16

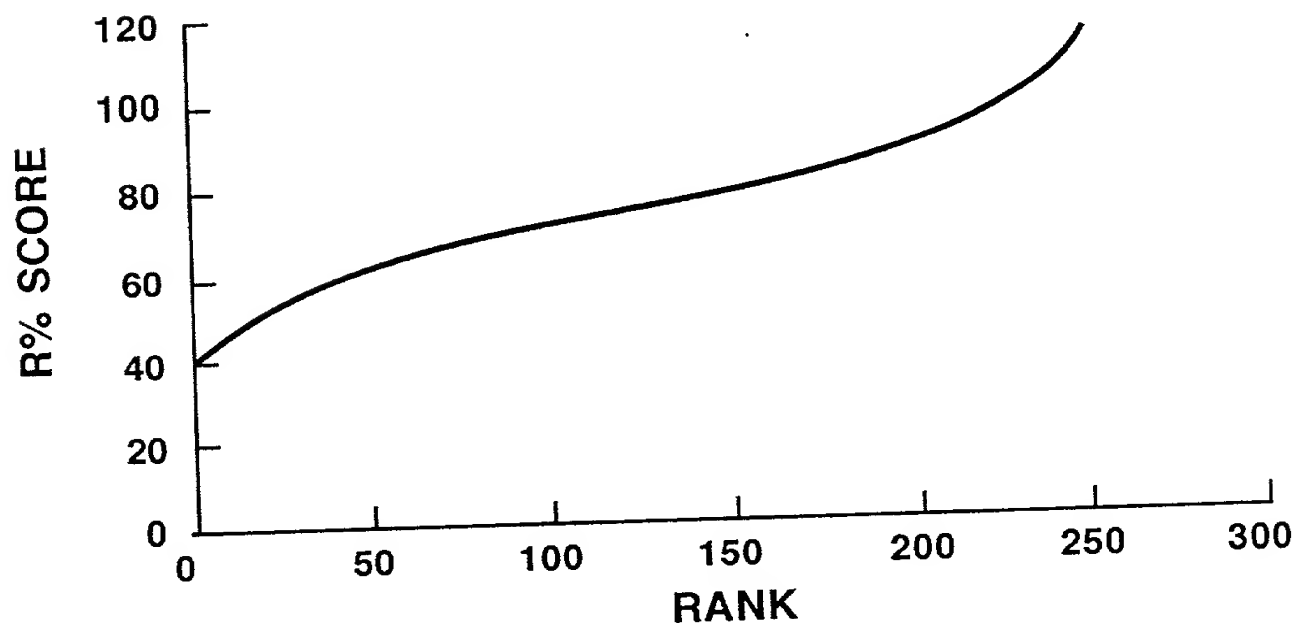


Fig. 17

Rank Order	oligo sequence	Screen A		Screen B		Screen C		Screen D		Screen E		Screen F		Screen G		Screen H		
		%R	Rank	%R	Rank	%R	Rank	%R	Rank	%R	Rank	%R	Rank	%R	Rank	%R	Rank	
1	155	GCGG	60.57	59	46.11	4	37.63	2	44.02	23	42.29	4	38.20	8	34.00	2	29.96	4
2	153	GCGA	39.38	5	58.55	13	48.16	8	53.50	42	55.55	23	45.91	17	34.13	4	23.44	2
3	145	GCAA	50.93	23	62.15	18	52.78	15	54.21	45	40.63	2	53.49	37	34.10	3	34.92	8
4	156	GCGT	60.46	57	67.86	32	N/A	N/A	43.71	22	54.34	20	27.70	1	36.75	5	30.84	6
5	151	GCCG	40.61	6	56.30	9	56.74	25	52.18	38	62.62	46	51.43	31	38.12	6	29.18	3
6	75	CAGG	44.18	13	66.99	30	56.07	24	42.54	20	60.96	43	45.78	15	52.39	30	38.96	12
7	146	GCAC	59.55	49	67.11	31	48.36	9	52.23	39	53.97	18	49.68	25	31.57	1	41.08	16
8	148	GCAT	48.01	20	44.74	3	47.41	7	37.09	13	48.95	10	72.50	113	46.77	17	30.33	5
9	149	GCCA	41.26	8	71.02	57	57.71	28	56.10	52	52.77	13	45.84	16	45.61	14	38.90	11
10	123	CTGG	41.41	9	47.23	5	52.90	16	38.33	15	57.05	27	45.98	18	63.29	95	54.06	51
11	150	GCCC	62.68	67	71.19	58	47.09	6	51.80	36	53.27	15	39.32	9	48.13	21	44.99	25
12	159	GCTG	52.56	28	75.16	89	68.03	67	35.56	11	50.54	12	42.24	12	45.75	15	36.09	10
13	171	GGGG	64.05	79	67.88	33	54.73	20	31.55	5	58.61	32	47.56	20	48.91	26	47.67	30
14	170	GGGC	59.34	47	69.04	47	64.46	51	48.86	28	54.20	19	49.88	26	44.85	12	44.06	22
15	90	CCGC	38.78	4	74.60	81	55.26	22	50.57	31	67.01	61	36.91	6	N/A	N/A	44.71	23
16	147	GCAG	60.36	54	78.98	126	51.43	13	48.35	27	41.47	3	N/A	N/A	42.29	9	17.89	1
17	160	GCTT	65.45	86	60.43	17	44.44	5	43.40	21	59.36	36	60.80	65	49.31	27	43.52	20
18	152	GCCT	66.55	91	58.49	12	N/A	N/A	46.77	25	59.52	38	59.72	61	39.45	7	39.31	15
19	161	GGAA	57.36	40	71.27	60	55.18	21	55.13	47	56.33	24	49.55	24	55.07	38	51.67	39
20	157	GCTA	59.75	51	75.10	87	61.83	39	53.52	43	56.75	25	53.54	38	43.75	11	39.02	13
21	84	CCAT	45.31	16	74.70	83	50.42	10	58.54	56	62.42	45	N/A	N/A	48.20	22	N/A	N/A
22	122	CTGC	43.98	12	84.23	168	25.02	1	33.34	7	59.29	34	52.36	34	54.94	37	44.90	24
23	158	GCTC	57.76	44	77.87	114	60.68	31	55.48	49	56.77	26	53.87	40	46.64	16	46.27	28
24	162	GGAC	55.84	35	64.55	23	61.23	36	50.92	34	66.79	58	62.93	71	59.85	70	54.50	52
25	194	TAAC	44.69	15	68.08	37	37.70	3	60.31	67	57.80	30	73.92	123	56.25	45	56.29	61

Fig. 18A(1)

26	154	GCGC	56.47	36	95.76	233	66.07	56	47.44	26	28.56	1	35.46	4	43.03	10	42.84	17
27	164	GGAT	60.37	55	77.48	112	51.38	12	55.13	48	63.83	50	52.73	35	55.54	39	49.89	33
28	174	GGTC	72.42	134	59.19	15	62.18	40	53.34	41	66.26	56	54.10	41	54.49	34	50.30	35
29	163	GGAG	59.48	48	72.78	72	65.90	54	60.50	68	65.59	54	62.54	70	56.87	48	42.89	18
30	119	CTCG	51.75	26	51.20	7	67.33	62	37.20	14	79.06	159	57.10	55	59.60	67	53.13	46
31	120	CTCT	60.01	52	63.68	22	53.91	18	27.93	2	110.40	237	44.83	13	47.47	19	58.88	78
32	176	GGTT	71.11	126	70.88	55	71.18	89	33.44	8	67.62	65	56.34	51	48.78	25	45.94	27
33	92	CCGT	41.58	10	31.15	1	66.84	58	63.24	89	73.85	116	68.91	88	61.63	80	50.58	36
34	74	CAGC	59.24	46	75.14	88	61.63	38	49.93	30	69.51	76	54.13	42	63.97	105	55.24	57
35	118	CTCC	61.32	61	39.91	2	160.43	230	49.60	29	44.22	6	57.04	54	58.85	62	52.10	40
36	195	TAAG	60.56	58	68.82	46	67.37	63	N/A	N/A	71.34	92	67.95	82	57.63	52	48.79	32
37	172	GGGT	68.78	106	51.13	6	N/A	N/A	N/A	N/A	78.73	158	62.08	68	45.43	13	39.11	14
38	97	CGAA	40.88	7	108.66	250	62.54	43	34.55	9	45.87	8	N/A	N/A	56.12	43	57.53	69
39	78	CATC	53.97	31	75.77	93	70.36	79	45.96	24	64.06	51	55.29	44	N/A	N/A	63.57	120
40	173	GGTA	70.86	120	72.53	69	54.30	19	50.71	33	71.76	97	38.16	7	72.85	186	51.58	38
41	190	GTTC	65.87	89	62.58	20	56.80	26	70.38	146	49.41	11	72.27	111	63.68	98	58.47	75
42	26	ACGC	68.19	102	70.11	51	65.99	55	38.55	16	67.75	66	87.20	203	53.17	31	54.69	53
43	94	CCTC	77.84	176	78.45	118	69.99	74	53.25	40	55.10	21	68.33	85	50.77	28	52.54	41
44	193	TAAA	62.35	65	66.98	29	62.47	42	81.83	220	48.32	9	72.13	107	41.67	8	63.60	121
45	98	CGAC	43.00	11	76.73	102	N/A	N/A	66.67	122	57.17	28	77.94	155	59.62	68	53.99	48
46	91	CCGG	37.67	3	77.48	111	N/A	N/A	60.54	69	52.81	14	N/A	N/A	79.40	222	52.95	44
47	243	TTAG	51.43	25	62.56	19	105.85	217	54.83	46	68.07	68	75.78	134	60.31	71	53.08	45
48	166	GGCC	63.70	76	83.98	164	55.83	23	73.29	176	53.29	16	47.93	22	60.94	74	61.57	101
49	244	TTAT	67.43	97	54.61	8	76.26	128	60.11	64	73.07	109	79.43	165	58.05	58	48.32	31
50	196	TAAT	78.47	179	66.80	28	51.75	14	N/A	N/A	69.98	79	82.49	185	56.19	44	55.14	55
51	82	CCAC	73.84	144	83.47	159	86.64	187	55.84	51	43.07	5	61.83	67	54.65	36	43.50	19
52	138	GAGC	65.53	88	84.11	165	71.29	91	60.24	66	58.70	33	41.87	11	69.61	152	57.12	67

Fig. 18A(2)

53	71	CACG	67.02	94	69.66	49	57.96	29	62.29	81	71.29	88	56.54	52	57.97	55	83.33	228
54	202	TAGC	81.74	206	83.44	158	74.12	110	30.93	4	57.63	29	51.92	33	53.78	32	62.78	111
55	250	TTGC	75.37	156	87.05	186	72.08	97	29.06	3	71.76	96	64.95	73	57.02	49	46.82	29
56	27	ACGG	66.61	92	80.03	133	71.62	93	67.29	126	45.40	7	81.44	180	57.66	53	34.56	7
57	57	ATGA	77.49	168	90.13	210	62.87	45	63.06	86	73.29	111	51.51	32	47.38	18	43.87	21
58	132	GAAT	73.50	141	86.93	184	62.25	41	56.35	53	77.91	153	33.80	3	59.09	64	55.79	59
59	251	TTGG	69.22	111	59.03	14	N/A	N/A	61.91	77	75.50	128	79.60	166	62.10	84	52.61	42
60	186	GTGC	50.43	22	77.20	105	N/A	N/A	77.04	198	N/A	N/A	55.38	45	61.30	77	60.15	88
61	180	GTAT	69.01	108	77.53	113	N/A	N/A	62.19	79	70.37	81	51.35	30	61.06	75	66.70	143
62	30	ACTC	63.85	78	71.43	61	76.78	133	73.84	180	72.55	104	55.77	47	61.40	78	53.99	49
63	4	AAAT	73.87	146	68.75	44	63.52	46	N/A	N/A	68.90	71	80.07	168	59.68	69	63.55	119
64	140	GAGT	65.50	87	68.60	43	81.50	168	68.10	131	55.38	22	72.01	106	69.75	154	56.56	62
65	31	ACTG	77.20	167	73.83	77	117.29	221	54.07	44	71.45	93	58.57	58	56.10	42	59.14	79
66	178	GTAC	61.36	62	71.74	63	93.90	205	64.94	103	60.33	41	69.14	89	66.03	126	61.09	98
67	175	GGTG	68.31	104	86.21	181	110.54	220	68.74	137	63.73	48	55.88	48	48.69	24	45.23	26
68	7	AACG	68.40	105	83.42	156	72.35	99	69.29	142	72.53	103	53.85	39	61.67	81	56.74	64
69	79	CATG	57.47	41	95.73	231	N/A	N/A	62.70	82	59.31	35	N/A	N/A	56.67	46	68.61	164
70	255	TTTG	71.02	122	102.27	247	64.12	50	59.40	61	59.82	39	72.54	114	63.90	102	57.10	66
71	29	ACTA	65.30	85	71.48	62	85.39	185	63.66	92	82.22	179	51.02	29	61.85	83	60.07	87
72	256	TTTT	73.85	145	88.88	200	72.92	104	60.98	71	60.55	42	76.19	138	56.85	47	55.49	58
73	77	CATA	45.90	17	76.72	101	63.84	47	62.16	78	67.89	67	N/A	N/A	74.86	200	76.18	199
74	83	CCAG	31.15	1	58.14	11	N/A	N/A	63.10	87	81.37	176	67.36	81	71.18	174	71.90	179
75	247	TTGG	69.06	109	60.09	16	166.33	231	68.62	136	74.92	122	59.22	60	57.85	54	60.23	90
76	76	CAGT	52.35	27	68.33	39	69.51	73	84.51	223	62.64	47	73.72	122	70.33	165	64.84	129
77	93	CCTA	51.13	24	89.50	207	70.81	85	65.38	107	N/A	N/A	47.85	21	74.06	194	59.98	85
78	18	ACAC	91.71	246	72.56	70	N/A	N/A	61.60	74	63.79	49	77.56	152	60.48	73	57.57	70
79	96	CCTT	67.50	98	87.74	192	80.15	160	35.55	10	75.52	129	N/A	N/A	55.86	41	N/A	N/A

Fig. 18A(3)

80	198	TACC	79.63	189	83.31	154	67.73	65	58.29	54	53.62	17	75.92	135	64.41	110	63.37	117
81	188	GTGT	66.82	93	65.68	27	N/A	N/A	60.60	70	83.11	186	76.88	144	67.53	137	59.33	80
82	131	GAAG	71.56	129	56.81	10	77.86	146	162.35	244	69.45	75	67.31	80	64.55	113	54.04	50
83	58	ATGC	79.53	187	82.93	151	103.10	216	63.78	94	61.71	44	46.36	19	51.19	29	62.86	113
84	10	AAGC	85.40	222	89.00	201	80.61	163	61.87	75	N/A	N/A	57.84	57	47.53	20	36.08	9
85	102	CGCC	63.63	75	78.60	120	71.74	94	69.04	140	85.17	199	63.39	72	57.14	50	N/A	N/A
86	179	GTAG	69.21	110	80.15	134	70.28	77	88.42	233	72.97	106	62.48	69	63.71	99	50.09	34
87	126	CTTC	70.58	116	75.24	90	73.83	108	61.26	72	72.59	105	53.06	36	77.14	214	63.83	122
88	253	TTTA	78.85	182	79.98	132	71.25	90	63.10	88	67.09	63	73.29	118	54.50	35	67.89	156
89	19	ACAG	77.59	173	74.85	86	78.05	149	62.96	85	70.40	82	77.05	146	58.01	56	60.51	92
90	66	CAAC	66.52	90	75.24	91	90.63	196	60.15	65	68.83	70	68.56	87	73.52	189	59.47	82
91	25	ACGA	47.26	19	71.84	64	77.06	137	62.81	84	84.75	196	N/A	N/A	58.05	57	77.52	209
92	99	CGAG	62.90	70	79.03	127	70.55	80	79.84	212	73.07	108	80.31	169	55.55	40	57.60	71
93	106	CGGC	69.82	112	68.07	36	96.25	210	63.80	95	70.03	80	77.45	150	58.37	59	66.06	139
94	133	GACA	70.88	121	75.86	95	66.91	59	71.95	165	65.72	55	N/A	N/A	61.56	79	76.62	203
95	221	TCTA	54.90	32	64.80	25	128.91	226	66.73	123	70.82	85	66.86	78	66.22	129	75.29	194
96	201	TAGA	73.16	140	70.43	53	75.52	119	69.57	144	69.31	73	88.58	205	65.38	119	52.93	43
97	107	CGGG	78.98	183	64.60	24	74.68	114	51.58	35	86.06	204	79.33	163	62.89	91	60.78	94
98	139	GAGG	68.24	103	76.19	97	83.24	178	66.31	118	58.16	31	N/A	N/A	70.92	169	61.10	99
99	169	GGGA	73.64	142	96.71	237	93.34	204	39.69	17	77.89	152	60.45	64	53.90	33	57.22	68
100	52	ATAT	75.03	154	68.77	45	66.77	57	62.26	80	68.39	69	68.12	83	86.84	243	74.43	187
101	129	GAAA	77.60	174	74.43	80	70.19	76	58.73	57	90.36	218	59.82	62	72.41	185	58.50	76
102	224	TCTT	61.96	63	74.26	79	76.77	132	71.36	157	67.08	62	76.59	142	63.23	94	76.19	200
103	87	CCCG	57.14	39	72.04	66	70.63	81	59.20	60	75.84	133	108.76	223	75.22	202	64.94	130
104	144	GATT	82.90	214	85.93	179	61.35	37	65.23	106	71.51	95	48.53	23	64.44	111	70.04	169
105	81	CCAA	60.24	53	81.34	141	66.98	60	73.43	177	83.02	185	32.30	2	66.46	130	74.45	188
106	241	TTAA	72.94	138	70.48	54	76.35	129	71.63	162	69.62	77	69.68	92	72.05	181	62.28	108

Fig. 18A(4)

107	100	CGAT	46.56	18	77.40	109	86.01	186	63.70	93	77.51	149	70.74	99	59.23	65	80.63	223
108	121	CTGA	44.48	14	95.99	235	N/A	N/A	59.19	59	87.65	211	N/A	N/A	62.57	86	61.75	104
109	64	ATTT	63.10	71	73.69	76	71.00	87	65.94	112	69.14	72	82.91	186	67.59	139	76.66	204
110	17	ACAA	89.62	238	78.08	116	74.84	117	63.95	96	70.74	84	60.39	63	63.63	96	66.99	145
111	189	GTTA	59.71	50	78.39	117	79.82	157	65.19	105	93.49	224	50.60	28	69.99	156	63.40	118
112	73	CAGA	64.95	83	83.20	153	67.48	64	67.89	130	75.69	130	N/A	N/A	64.18	107	71.02	173
113	70	CACC	77.50	169	70.23	52	93.28	203	N/A	N/A	66.61	57	97.69	215	58.76	61	59.99	86
114	218	TCGC	97.46	252	77.27	107	60.99	34	78.02	205	N/A	N/A	68.42	86	58.94	63	61.07	97
115	124	CTGT	70.70	117	84.59	172	71.31	92	64.69	101	76.75	141	66.15	77	67.51	136	65.74	134
116	101	CGCA	64.43	81	77.35	108	70.35	78	84.56	224	80.07	165	76.11	137	57.21	51	64.98	131
117	59	ATGG	79.34	186	138.30	254	57.31	27	59.53	62	94.28	226	36.05	5	65.84	125	60.87	95
118	184	GTCT	55.42	33	81.97	144	80.96	165	105.72	241	N/A	N/A	44.89	14	69.67	153	62.33	109
119	167	GGCG	71.79	130	72.81	73	81.64	169	84.48	222	71.87	98	72.24	109	64.25	108	59.66	83
120	191	GTTG	61.96	64	82.68	149	83.67	180	84.99	226	78.55	157	40.73	10	70.21	162	53.17	47
121	222	TCTC	56.59	37	73.49	75	N/A	N/A	88.12	232	74.72	121	69.89	95	67.43	135	71.74	177
122	28	ACGT	62.71	68	68.36	40	71.00	88	63.29	90	110.06	236	71.53	104	80.50	225	67.45	150
123	249	TTGA	56.92	38	71.87	65	82.61	175	N/A	N/A	87.81	212	77.68	153	65.36	118	63.20	116
124	177	GTAA	74.68	152	76.05	96	82.21	171	67.64	128	87.60	209	69.79	93	63.18	93	57.09	65
125	80	CATT	53.28	30	85.96	180	76.72	130	65.92	111	75.23	125	72.55	115	70.13	160	69.02	166
126	187	GTGG	49.60	21	98.27	242	108.71	219	74.66	184	73.09	110	54.24	43	67.14	131	58.25	73
127	245	TTCA	57.49	42	84.27	170	79.74	156	33.20	6	82.51	182	70.50	97	68.34	142	84.81	231
128	62	ATTC	77.57	172	82.26	146	70.69	83	59.98	63	77.00	144	50.17	27	71.98	178	80.17	221
129	165	GGCA	60.85	60	85.87	177	77.38	141	50.70	32	95.68	230	65.20	75	78.36	218	61.68	102
130	203	TAGG	83.46	218	63.09	21	75.82	121	71.34	155	71.94	99	71.05	101	64.32	109	78.89	216
131	199	TACG	80.64	197	71.25	59	68.65	70	66.59	120	103.91	234	59.12	59	107.68	248	55.14	54
132	50	ATAC	79.80	191	84.11	166	66.98	61	79.99	215	80.63	170	55.61	46	62.89	90	61.75	103
133	246	TTCC	73.71	143	78.62	121	82.12	170	79.89	213	77.01	145	71.50	103	48.57	23	64.70	128
134	130	GAAC	72.36	132	83.69	160	124.36	225	71.56	161	67.35	64	73.07	116	64.67	115	58.40	74

Fig. 18A(5)

135	33	AGAA	70.76	118	70.89	56	77.15	138	42.19	19	81.86	177	91.67	209	84.34	233	61.18	100
136	114	CTAC	70.20	114	77.21	106	N/A	N/A	71.81	164	72.23	101	71.39	102	73.41	188	66.85	144
137	32	ACTT	71.10	125	76.57	99	75.96	123	72.19	167	74.96	123	65.31	76	72.31	183	67.96	157
138	137	GAGA	67.88	101	90.21	214	68.49	69	27.69	1	59.49	37	101.67	218	70.28	164	116.99	249
139	110	CGTC	75.37	158	90.14	211	60.78	32	64.62	99	76.01	135	72.24	110	70.41	167	66.33	142
140	205	TATA	76.38	165	78.80	125	64.00	48	68.41	133	78.22	155	81.07	175	N/A	N/A	65.13	132
141	219	TCGG	75.75	162	78.79	124	77.75	144	85.57	228	80.79	172	61.80	66	64.05	106	58.22	72
142	54	ATCC	87.49	233	85.52	175	N/A	N/A	55.49	50	84.75	197	69.39	90	62.58	88	62.26	107
143	3	AAAG	74.56	151	139.01	255	71.76	95	72.23	168	69.81	78	76.46	141	65.79	124	56.63	63
144	252	TTGT	74.55	150	90.30	215	75.85	122	65.62	109	N/A	N/A	75.12	129	59.40	66	67.54	152
145	46	AGTC	72.75	136	81.56	143	80.26	161	65.45	108	71.20	87	87.74	204	65.73	123	64.30	125
146	168	GGCT	74.25	147	81.52	142	50.55	11	73.26	175	73.86	117	67.19	79	80.70	226	75.37	195
147	208	TATT	88.36	236	73.98	78	70.11	75	65.10	104	73.70	115	81.39	179	69.39	151	67.87	155
148	185	GTGA	59.16	45	94.17	228	83.61	179	51.86	37	114.85	238	56.26	50	68.56	147	70.16	170
149	95	CCTG	60.41	56	72.75	71	79.13	154	66.06	115	N/A	N/A	86.62	199	86.12	239	64.49	127
150	89	CCGA	33.81	2	83.89	163	N/A	N/A	77.77	204	64.97	52	71.83	105	74.05	193	95.06	244
151	242	TTAC	71.05	123	68.46	42	76.73	131	74.29	182	77.10	146	78.77	158	67.56	138	73.88	186
152	49	ATAA	90.67	243	75.72	92	72.47	100	78.06	206	78.40	156	N/A	N/A	64.56	114	56.07	60
153	11	AAGG	77.83	175	67.92	35	74.69	115	72.74	172	87.62	210	80.45	170	61.13	76	68.56	163
154	9	AAGA	79.67	190	87.30	189	70.90	86	71.17	152	76.63	139	98.05	216	63.03	92	55.16	56
155	63	ATTG	67.08	95	93.18	223	72.20	98	64.04	97	74.11	118	83.70	187	68.98	148	68.14	158
156	105	CGGA	82.96	215	72.33	68	72.83	103	74.96	186	88.16	214	N/A	N/A	58.40	60	66.05	138
157	192	GTTT	63.61	74	98.11	241	139.09	228	63.49	91	125.14	240	56.74	53	62.74	89	62.54	110
158	207	TATG	79.23	185	90.15	212	59.59	30	74.94	185	74.35	119	74.77	126	68.54	146	64.20	124
159	51	ATAG	93.62	249	87.02	185	65.34	52	68.45	134	75.90	134	102.67	220	65.02	117	50.60	37
160	135	GACG	75.37	157	78.50	119	82.57	174	61.50	73	76.79	142	86.71	201	69.99	157	61.89	105
161	209	TCAA	80.79	198	81.32	140	60.93	33	76.22	193	70.48	83	75.34	131	69.32	150	76.40	201

Fig. 18A(6)

162	20	ACAT	90.38	241	88.41	196	69.38	72	70.27	145	71.98	100	74.35	125	66.20	128	64.05	123
163	230	TGCC	63.40	73	73.36	74	84.01	182	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	87.55	236
164	22	ACCC	69.83	113	84.20	167	360.73	232	40.14	18	67.00	60	81.62	183	70.05	158	76.84	205
165	104	CGCT	82.57	212	74.62	82	94.87	207	72.49	171	78.21	154	73.70	121	62.50	85	63.06	114
166	197	TACA	80.55	195	88.11	195	64.01	49	84.73	225	65.51	53	76.00	136	65.44	121	71.63	175
167	6	AACC	80.18	192	93.97	225	N/A	N/A	71.52	160	72.97	107	N/A	N/A	63.67	97	59.42	81
168	183	GTCG	53.05	29	79.84	131	95.24	208	69.04	139	90.32	217	70.64	98	70.07	159	70.96	172
169	65	CAAA	62.52	66	78.65	123	82.95	176	71.47	159	73.47	112	77.24	147	71.90	177	75.43	196
170	53	ATCA	77.99	177	89.12	203	73.53	106	62.74	83	76.35	136	72.15	108	65.43	120	84.40	230
171	67	CAAG	72.17	131	107.82	249	76.00	125	66.06	114	71.31	90	N/A	N/A	69.88	155	67.72	154
172	206	TATC	77.57	171	89.46	206	62.84	44	75.93	189	60.27	40	76.34	139	76.75	210	69.56	167
173	36	AGAT	80.96	201	75.78	94	53.13	17	70.42	147	76.36	137	83.92	188	74.06	195	74.52	189
174	103	CGCG	125.02	255	72.32	67	80.36	162	67.56	127	97.53	231	N/A	N/A	63.89	101	59.86	84
175	128	CTTT	72.98	139	87.83	193	72.04	96	58.86	58	89.18	216	72.37	112	83.53	231	65.66	133
176	200	TACT	87.43	232	65.63	26	67.96	66	79.20	209	80.78	171	80.56	172	74.16	196	61.91	106
177	220	TCGT	87.10	230	79.06	128	83.88	181	66.97	125	72.39	102	79.15	162	64.48	112	N/A	N/A
178	211	TCAG	81.49	204	90.60	217	79.92	158	66.02	113	75.78	132	74.83	128	67.31	134	62.85	112
179	223	TC TG	72.42	135	95.29	230	91.12	198	74.14	181	69.37	74	75.15	130	63.92	103	67.58	153
180	16	AATT	84.54	220	69.46	48	78.00	148	66.60	121	77.27	147	74.02	124	75.56	204	77.01	207
181	111	CGTG	75.03	155	82.01	145	68.12	68	68.50	135	79.35	162	73.27	117	73.68	191	99.19	246
182	125	CTTA	70.81	119	81.09	139	73.96	109	67.71	129	N/A	N/A	N/A	N/A	71.71	176	99.86	247
183	60	ATGT	80.44	194	84.45	171	44.43	4	70.75	150	82.79	183	75.41	132	90.44	247	67.00	146
184	210	TCAC	63.73	77	76.53	98	79.92	159	36.31	12	104.55	235	92.68	212	78.24	217	78.90	217
185	141	GATA	95.02	250	74.84	85	91.21	199	N/A	N/A	74.53	120	73.29	119	76.49	208	60.61	93
186	34	AGAC	78.50	180	79.13	129	101.67	215	71.63	163	71.47	94	79.05	161	67.18	132	68.46	160
187	204	TAGT	91.18	245	84.25	169	92.03	201	72.26	169	66.86	59	69.40	91	68.99	149	68.61	165
188	181	GTCA	114.04	254	83.39	155	100.90	214	61.90	76	84.12	190	74.78	127	62.57	87	67.42	149

Fig. 18A(7)

189	142	GATC	72.41	133	89.04	202	87.57	192	70.76	151	75.33	126	86.29	197	70.13	161	60.39	91
190	116	CTAT	80.41	193	96.23	236	77.22	139	N/A	N/A	70.87	86	76.94	145	71.01	172	64.33	126
191	42	AGGC	72.91	137	81.02	137	N/A	N/A	79.09	208	87.53	208	57.36	56	85.93	238	63.20	115
192	1	AAAA	87.21	231	78.63	122	77.71	143	68.37	132	87.37	205	N/A	N/A	66.09	127	66.30	141
193	134	GACC	77.53	170	67.89	34	148.56	229	69.47	143	83.83	189	77.31	149	70.25	163	72.45	182
194	254	TTTC	80.58	196	89.83	209	N/A	N/A	66.43	119	76.70	140	80.53	171	63.79	100	70.39	171
195	117	CTCA	86.48	228	83.86	162	76.84	134	64.64	100	98.87	232	81.15	176	68.49	145	61.01	96
196	136	GACT	80.80	199	125.62	253	75.66	120	72.33	170	80.16	166	70.97	100	73.65	190	58.85	77
197	115	CTAG	75.57	161	103.17	248	77.36	140	69.02	138	N/A	N/A	N/A	N/A	67.27	133	66.00	137
198	72	CACT	75.54	159	84.94	174	N/A	N/A	75.76	188	75.12	124	N/A	N/A	61.70	82	85.97	232
199	15	AATG	90.31	240	91.51	219	70.79	84	71.42	158	76.96	143	78.95	160	68.18	141	65.78	135
200	143	GATG	82.18	209	77.08	104	82.35	172	75.16	187	N/A	N/A	56.13	49	70.94	170	83.55	229
201	61	ATTA	86.48	227	87.73	191	75.97	124	71.18	153	73.55	113	N/A	N/A	60.48	72	91.80	241
202	35	AGAG	80.89	200	68.45	41	87.40	191	64.52	98	80.52	168	81.53	182	75.82	206	78.70	214
203	85	CCCA	88.24	235	85.91	178	81.43	167	58.51	55	73.63	114	N/A	N/A	72.00	180	78.82	215
204	68	CAAT	70.31	115	90.37	216	80.88	164	71.31	154	77.69	150	81.51	181	71.16	173	68.53	161
205	14	AATC	90.09	239	89.40	205	68.88	71	70.66	148	81.08	174	78.27	157	72.36	184	66.14	140
206	248	TTCT	67.84	100	68.10	38	90.96	197	N/A	N/A	84.50	192	84.60	190	109.00	249	74.60	190
207	182	GTCC	76.24	164	69.74	50	132.12	227	64.83	102	84.98	198	86.52	198	75.68	205	75.46	198
208	13	AATA	93.48	248	82.69	150	84.97	184	66.82	124	84.59	193	N/A	N/A	63.92	104	72.93	184
209	86	CCCC	65.16	84	93.13	222	117.51	222	77.01	197	80.61	169	64.99	74	73.22	187	76.55	202
210	55	ATCG	88.83	237	82.62	148	121.85	224	70.70	149	80.06	164	N/A	N/A	65.49	122	67.16	148
211	109	CGTA	74.47	148	222.74	256	65.82	53	76.48	194	92.66	221	N/A	N/A	68.45	143	71.90	178
212	227	TGAG	62.76	69	93.96	224	73.79	107	77.12	200	86.01	203	85.01	193	73.72	192	71.94	181
213	127	CTTG	67.24	96	95.73	232	77.04	136	76.63	195	80.43	167	N/A	N/A	77.03	213	68.53	162
214	56	ATCT	79.60	188	98.81	243	97.66	212	95.73	238	75.40	127	76.35	140	67.91	140	60.20	89

Fig. 18A(8)

215	8	AACT	63.39	72	89.56	208	78.72	152	133.37	243	N/A	N/A	82.01	184	71.98	179	71.48	174
216	39	AGCG	55.62	34	81.03	138	90.52	195	N/A	N/A	94.55	227	98.66	217	78.60	219	73.52	185
217	217	TCGA	74.55	149	87.65	190	70.63	82	80.91	218	87.39	206	76.72	143	74.91	201	78.18	210
218	113	CTAA	81.74	207	82.35	147	74.43	113	73.65	179	79.49	163	116.48	225	68.47	144	81.07	224
219	237	TGTA	78.22	178	74.76	84	120.76	223	80.70	217	71.33	91	79.83	167	80.22	224	80.00	220
220	225	TGAA	81.19	202	83.42	157	84.02	183	85.37	227	77.75	151	69.80	94	76.65	209	72.75	183
221	69	CACA	78.67	181	91.38	218	74.72	116	69.10	141	82.23	180	85.55	194	75.46	203	N/A	N/A
222	112	CGTT	76.02	163	92.06	220	78.20	150	77.13	201	85.76	201	69.94	96	77.00	212	N/A	N/A
223	88	CCCT	64.56	82	83.70	161	72.52	102	89.96	234	82.17	178	92.41	211	132.23	251	76.87	206
224	23	ACCG	92.45	247	79.82	130	83.22	177	72.11	166	79.16	160	75.57	133	72.05	182	86.09	233
225	2	AAAC	86.91	229	86.72	183	77.79	145	76.12	192	85.50	200	81.04	174	70.95	171	65.85	136
226	212	TCAT	82.25	210	100.54	244	74.42	112	81.54	219	79.31	161	85.85	195	64.89	116	71.69	176
227	5	AACA	82.03	208	102.03	246	76.87	135	71.35	156	71.29	89	95.87	214	N/A	N/A	77.15	208
228	47	AGTG	68.89	107	83.05	152	89.02	194	78.89	207	82.81	184	81.22	177	83.88	232	75.15	192
229	214	TCCC	88.19	234	77.05	103	78.22	151	76.96	196	75.69	131	N/A	N/A	89.31	246	78.25	212
230	215	TCCG	90.57	242	80.30	135	82.42	173	73.62	178	76.58	138	89.79	207	80.86	227	68.31	159
231	38	AGCC	86.33	226	77.43	110	87.33	189	80.43	216	83.60	188	78.21	156	77.19	215	69.96	168
232	234	TGGC	64.41	80	88.50	198	N/A	N/A	72.86	173	82.32	181	84.96	192	86.57	241	80.18	222
233	45	AGTA	71.40	128	77.89	115	81.38	166	77.24	202	88.91	215	104.60	222	84.62	234	78.19	211
234	228	TGAT	85.64	223	87.88	194	76.05	126	79.93	214	N/A	N/A	78.86	159	70.36	166	91.45	239
235	213	TCCA	91.13	244	101.29	245	61.15	35	79.36	210	N/A	N/A	85.98	196	74.48	199	75.26	193
236	108	CGGT	83.16	217	90.19	213	73.16	105	104.86	240	93.95	225	79.38	164	70.58	168	75.10	191

Fig. 18A(9)

237	229	TGCA	71.23	127	87.23	187	79.15	155	87.74	231	87.87	213	77.48	151	86.70	242	79.41	218
238	37	AGCA	83.10	216	85.57	176	87.39	190	66.12	116	90.83	220	N/A	N/A	74.37	197	79.91	219
239	239	TGTG	76.41	166	94.15	227	N/A	N/A	77.07	199	77.32	148	110.58	224	84.72	235	67.09	147
240	231	TGGG	74.69	153	86.37	182	87.30	188	91.97	237	80.94	173	80.57	173	78.96	221	78.64	213
241	226	TGAC	84.64	221	89.18	204	106.84	218	76.03	191	94.57	228	73.50	120	76.82	211	67.50	151
242	236	TGGT	79.11	184	76.66	100	97.31	211	N/A	N/A	81.30	175	102.37	219	82.29	229	87.08	235
243	232	TGCT	57.69	43	95.24	229	91.54	200	82.10	221	84.29	191	91.86	210	83.35	230	83.14	227
244	24	ACCT	96.57	251	84.93	173	76.14	127	73.03	174	90.46	219	84.26	189	74.46	198	87.02	234
245	41	AGGA	81.23	203	93.99	226	77.53	142	91.66	236	93.02	223	68.22	84	113.69	250	90.63	238
246	44	AGGT	83.59	219	80.67	136	94.43	206	65.83	110	95.29	229	104.27	221	86.47	240	92.25	242
247	43	AGGG	86.24	225	97.24	239	N/A	N/A	66.15	117	87.41	207	77.87	154	79.81	223	91.72	240
248	21	ACCA	135.86	256	97.64	240	74.90	118	76.00	190	84.70	195	86.68	200	80.99	228	71.92	180
249	233	TGGA	71.07	124	110.33	252	92.16	202	79.48	211	N/A	N/A	77.27	148	87.17	244	82.74	226
250	40	AGCT	67.69	99	87.27	188	95.79	209	86.79	229	102.52	233	93.53	213	89.04	245	75.44	197
251	12	AAGT	81.66	205	92.86	221	74.22	111	107.95	242	N/A	N/A	89.87	208	71.18	175	118.83	250
252	48	AGTT	82.33	211	96.83	238	87.79	193	74.41	183	83.59	187	81.39	178	78.87	220	81.71	225
253	235	TGGG	75.55	160	88.44	197	98.72	213	96.03	239	85.88	202	84.86	191	85.53	237	88.22	237
254	238	TGTC	85.93	224	88.81	199	78.81	153	77.37	203	118.62	239	N/A	N/A	77.66	216	103.38	248
255	216	TCCT	100.46	253	95.84	234	72.52	101	91.36	235	92.72	222	88.88	206	76.37	207	94.84	243
256	240	TGTT	82.60	213	110.20	251	77.91	147	86.95	230	84.66	194	87.10	202	85.39	236	95.58	245

Fig. 18A(10)

Average %bound	Average Rank	Rank Order	oligo
41.60	13	1	155
44.83	14	2	153
47.90	19	3	145
45.95	20	4	156
48.40	21	5	151
50.98	23	6	75
50.44	24	7	148
46.98	24	8	148
51.15	25	9	149
50.03	30	10	123
52.31	30	11	150
50.74	31	12	159
52.62	31	13	171
54.33	32	14	170
52.55	33	15	90
48.68	33	16	147
53.34	35	17	160
52.83	36	18	152
56.44	37	19	161
55.41	38	20	157
56.60	39	21	84
49.76	40	22	122
56.92	44	23	158
59.58	47	24	162
56.88	48	25	194
51.95	48	26	154
58.29	48	27	164
59.04	50	28	174
60.82	54	29	163
57.05	55	30	119
58.39	55	31	120
58.16	56	32	176

Fig. 18B(1)

57.22	60	33	92
61.10	60	34	74
65.43	61	35	118
63.21	61	36	195
57.54	61	37	172
58.02	61	38	97
61.28	63	39	78
60.34	71	40	173
62.43	72	41	190
63.21	72	42	26
63.28	73	43	94
62.42	75	44	193
62.16	76	45	98
60.14	77	46	91
66.49	78	47	243
62.57	82	48	166
64.66	83	49	244
65.83	83	50	196
62.85	84	51	82
63.56	84	52	138
65.76	85	53	71
62.04	85	54	202
63.01	86	55	250
63.08	86	56	27
63.70	86	57	57
63.20	87	58	132
65.71	89	59	251
63.58	89	60	186
65.46	90	61	180
66.20	91	62	30
68.33	95	63	4
67.17	97	64	140
70.95	98	65	31
68.57	98	66	178

Fig. 18B(2)

SECRET

68.42	99	67	175
67.28	99	68	7
66.75	100	69	79
68.77	100	70	255
67.62	100	71	29
68.21	101	72	256
66.79	101	73	77
63.46	101	74	83
77.04	102	75	247
68.28	103	76	76
65.53	103	77	93
69.32	105	78	18
67.05	105	79	96
68.28	105	80	198
68.56	105	81	188
77.99	106	82	131
68.93	107	83	58
65.48	107	84	10
69.82	107	85	102
69.66	108	86	179
68.44	108	87	126
69.49	108	88	253
69.93	108	89	19
70.36	109	90	66
68.47	109	91	25
69.86	110	92	99
71.23	110	93	106
69.93	111	94	133
74.32	112	95	221
70.61	112	96	201
69.86	114	97	107
69.17	114	98	139
69.10	115	99	169
71.33	115	100	52

Fig. 18B(3)

70.26	116	101	129
70.93	116	102	224
72.97	117	103	87
68.74	117	104	144
67.28	117	105	81
70.63	118	106	241
70.22	118	107	100
68.61	118	108	121
71.25	118	109	64
71.03	119	110	17
70.07	119	111	189
70.63	120	112	73
74.87	120	113	70
71.74	121	114	218
70.93	121	115	124
71.88	122	116	101
73.94	123	117	59
71.57	123	118	184
72.34	124	119	167
69.49	124	120	191
71.71	125	121	222
74.36	125	122	28
72.21	125	123	249
72.28	126	124	177
71.10	127	125	80
73.00	128	126	187
70.11	128	127	245
71.23	129	128	62
71.96	129	129	165
72.49	130	130	203
76.62	130	131	199
71.47	130	132	50
72.01	131	133	248
76.93	131	134	130

Fig. 18B(4)

72.50	131	135	33
71.87	131	136	114
72.05	132	137	32
75.34	132	138	137
71.99	132	139	110
73.14	133	140	205
72.84	134	141	219
72.50	134	142	54
78.28	134	143	3
72.63	135	144	252
73.63	136	145	46
72.09	137	146	168
73.74	137	147	208
74.83	137	148	185
73.86	137	149	95
71.62	138	150	89
73.48	138	151	242
73.70	139	152	49
73.87	140	153	11
75.24	140	154	9
73.93	141	155	63
73.67	141	156	105
83.93	141	157	192
73.22	141	158	207
76.08	141	159	51
74.17	141	160	135
73.85	141	161	209
74.38	141	162	20
77.08	141	163	230
106.30	142	164	22
75.25	143	165	104
74.50	144	166	197
73.62	144	167	6
74.89	144	168	183

Fig. 18B(5)

74.20	145	169	65
75.21	145	170	53
75.85	145	171	67
73.59	146	172	206
73.64	146	173	36
80.93	147	174	103
75.31	147	175	128
74.70	147	176	200
76.15	148	177	220
74.85	150	178	211
76.13	151	179	223
75.31	152	180	16
77.39	152	181	111
77.52	153	182	125
74.46	153	183	60
76.36	153	184	210
78.00	153	185	141
77.14	154	186	34
76.70	156	187	204
81.14	157	188	181
76.49	157	189	142
76.71	157	190	116
75.29	157	191	42
75.95	157	192	1
83.41	157	193	134
75.46	158	194	254
77.67	159	195	117
79.75	159	196	136
76.40	160	197	115
76.50	160	198	72
76.74	160	199	15
75.34	160	200	143
78.17	160	201	61
77.23	163	202	35

Fig. 18B(6)

76.93	163	203	85
78.47	164	204	68
77.11	165	205	14
82.80	165	206	248
83.20	168	207	182
78.49	170	208	13
81.02	170	209	86
82.38	170	210	55
96.08	170	211	109
78.04	171	212	227
77.52	172	213	127
81.46	172	214	56
84.36	173	215	8
81.78	174	216	39
78.87	175	217	217
82.21	175	218	113
83.23	176	219	237
78.87	176	220	225
79.59	176	221	69
79.44	178	222	112
86.80	178	223	88
80.06	179	224	23
78.86	179	225	2
80.06	179	226	212
82.37	179	227	5
80.36	181	228	47
80.52	182	229	214
80.30	182	230	215
80.06	184	231	38
79.97	184	232	234
83.03	187	233	45
81.45	189	234	228
81.24	189	235	213
83.80	190	236	108

82.10	191	237	229
81.04	191	238	37
83.81	192	239	239
82.43	193	240	231
83.63	193	241	226
86.59	193	242	236
83.65	194	243	232
83.36	196	244	24
88.75	200	245	41
87.85	200	246	44
83.78	201	247	43
88.59	201	248	21
85.75	201	249	233
87.26	202	250	40
90.94	202	251	12
83.36	204	252	48
87.90	210	253	235
90.08	212	254	238
89.13	213	255	216
88.80	215	256	240

Fig. 18B(8)

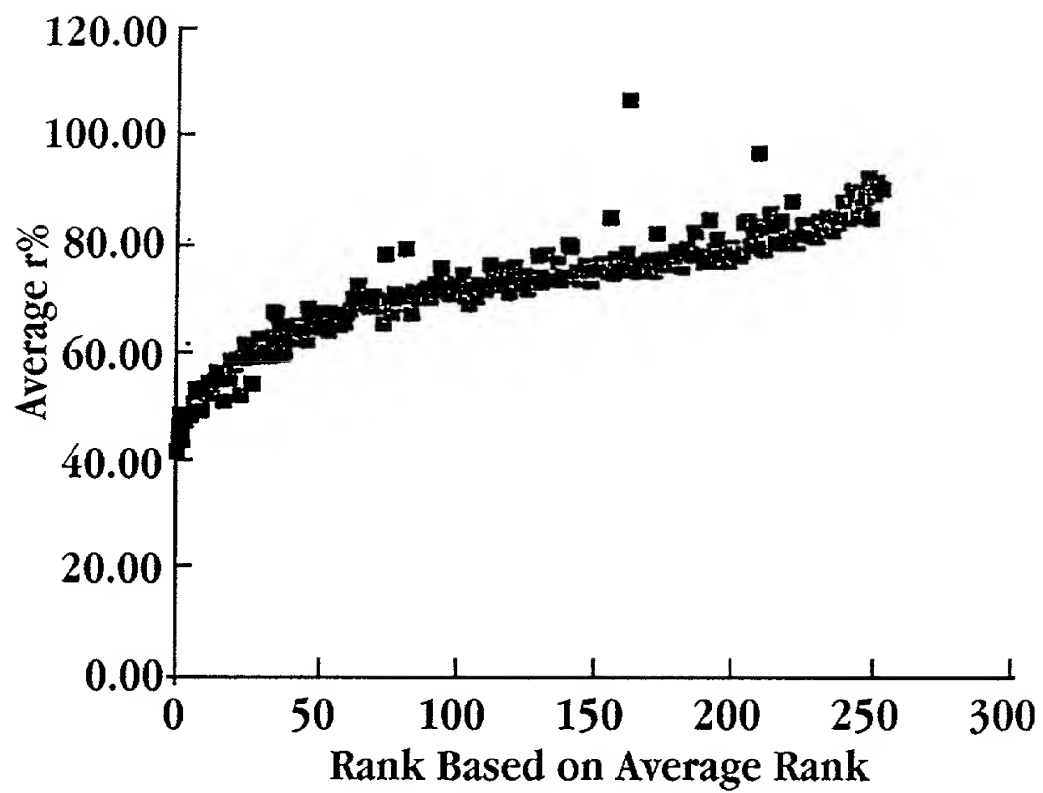


Fig. 19

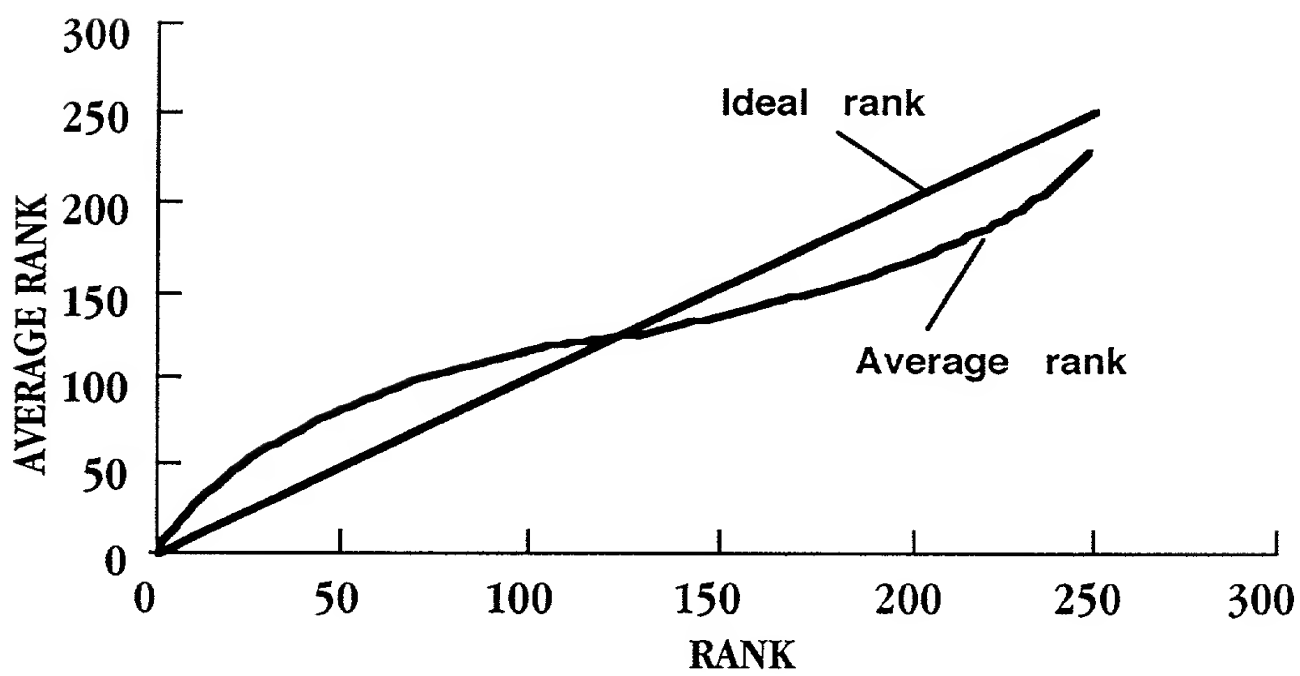


Fig. 20

Actinomycin D: Variance from mean	
A1	-4.38
C1	1.09
G1	7.71
T1	-4.42
A2	-0.29
C2	4.39
G2	-4.02
T2	-0.08
A3	2.29
C3	-4.88
G3	2.86
T3	-0.27
A4	-0.92
C4	2.01
G4	0.56
T4	-1.65

Fig. 21

	N1N2	N1N3	N1N4	N2N3	N2N4	N3N4	XNX	XX
AA	-3.39	-0.94	-4.21	0.80	-2.00	2.56	-1.47	-0.01
AC	-3.00	-10.57	-2.04	-3.61	2.28	1.72	-4.14	-1.63
AG	-10.85	-2.35	-3.13	2.14	0.89	1.29	-0.73	-2.47
AT	-0.25	-3.64	-8.12	-0.49	-2.33	3.58	-2.98	0.95
CA	1.52	1.61	-1.63	7.80	3.78	-3.33	2.69	2.00
CC	2.14	-2.89	4.97	-4.43	4.63	-5.45	0.87	-2.58
CG	-1.38	5.44	2.58	8.94	5.72	-3.56	5.58	1.33
CT	2.08	0.20	-1.55	5.26	3.44	-7.19	1.82	0.05
GA	-1.48	9.81	6.63	1.08	-3.47	-1.31	3.17	-0.57
GC	23.80	2.40	7.64	-7.41	-1.51	9.80	0.44	8.73
GG	10.42	11.66	7.28	-4.76	-4.87	5.21	3.39	3.62
GT	-1.89	6.96	9.30	-5.00	-6.22	-2.27	0.37	-3.05
TA	2.19	-1.33	-4.47	-0.54	-1.99	-1.60	-1.66	0.02
TC	-5.36	-8.47	-2.54	-4.07	2.63	1.95	-2.92	-2.49
TG	-14.27	-3.31	-4.46	5.12	0.52	-0.69	-1.39	-3.28
TT	-0.26	-4.59	-6.22	-0.84	-1.49	-0.72	-3.04	-0.61
stdev:	8.44	6.13	5.54	4.86	3.52	4.22	2.78	3.04

Fig. 22

Figure 23 shows the results of the analysis of the data from the experiment described in Figure 22. The data are presented in the form of a bar chart, with the y-axis representing the value of the function and the x-axis representing the sequence of the data. The legend indicates that the bars represent the values of the function for the different sequences of the data.

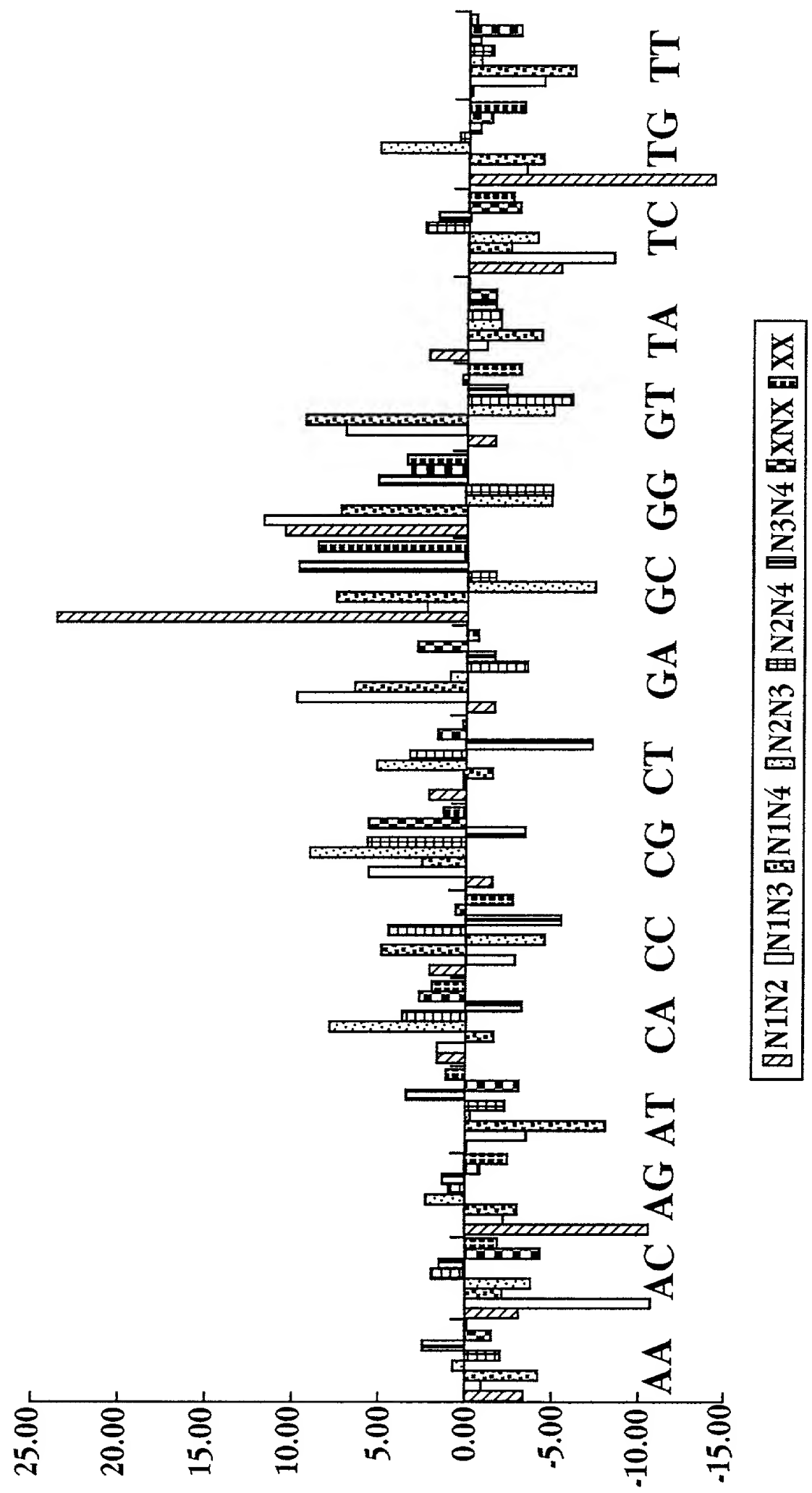


Fig. 23

Figure 24: A bar chart showing the distribution of various categories (AA to TT) across different groups (N1N2 to XX). The Y-axis represents values from -30.00 to 60.00. The legend identifies the groups by their fill patterns.

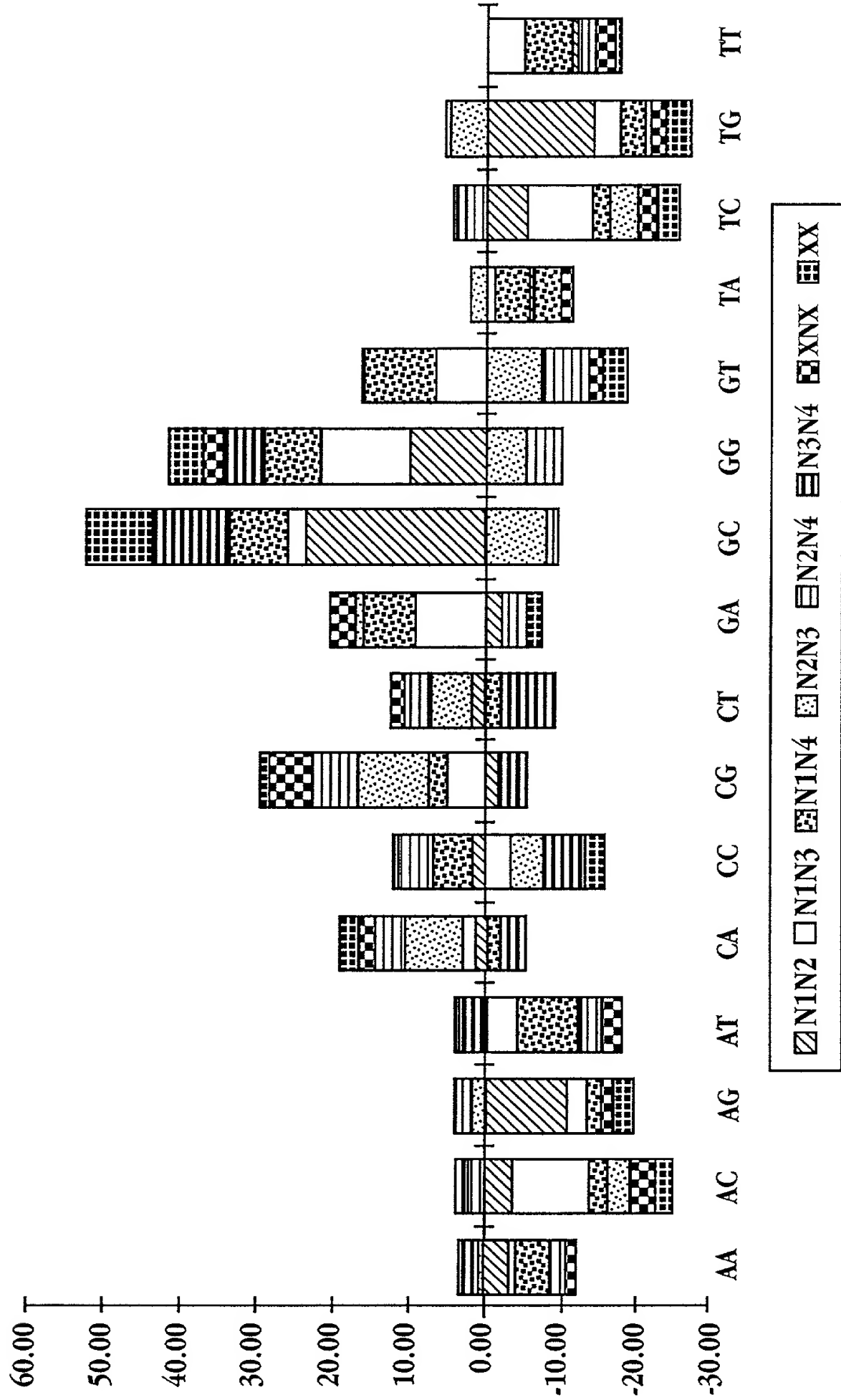


Fig. 24

TTCCTTCC	TTACTTCC	TACCTTCC	TAACCTCC
TTCCTTAC	TTACTTAC	TACCTTAC	TAACCTAC
TTCCTACC	TTACTACC	TACCTACC	TAACCTACC
TTCCTAAC	TTACTAAC	TACCTAAC	TAACCTAAC

Fig. 25

Fig. 26

TTCCNTTCC
TTCCNNTTCC
TTCCNNNTTCC
TTCCNNNNTTCC

- → - UL9 → - →
 5' -GCGTANXYZZCGTTTCGCACTTXYZZCTTCGTCCCAAT-3' Score
 3' -CGCATNYXQQGCAAGCGTGAAYXQQGAAGCAGGGTTA-5' high

Fig. 27A

-UL9 →
 5' -GCGTANQQXYCGTTTCGCACTTQQXYCTTCGTCCCAAT-3' Score
 3' -CGCATNZZYXGCAAGCGTGAZZZYXGAAGCAGGGTTA-5' low

Fig. 27B

- → - →
 5' -GCGTANXYZZAAGTGCGAACGXYZZCTTCGTCCCAAT-3'
 3' -CGCATNYXQQTTCACGCTTGCYXQQGAAGCAGGGTTA-5'
 ← -UL9- -

Fig. 27C

5' -GCGTANQQXYAAGTGCGAACGQQXYCTTCGTCCCAAT-3'
 3' -CGCATNZZYXTTCACGCTTGCZZZYXGAAGCAGGGTTA-5'
 ← - ← -UL9- - ← -

Fig. 27D

- → - UL9 →
 5' -GCGTANXYZZCGTTTCGCACTTQQXYCTTCGTCCCAAT-3'
 3' -CGCATNYXQQGCAAGCGTGAZZZYXGAAGCAGGGTTA-5'
 ← -

Fig. 27E

- UL9 → - →
 5' -GCGTANQQXYCGTTTCGCACTTXYZZCTTCGTCCCAAT-3'
 3' -CGCATNZZYXGCAAGCGTGAAYXQQGAAGCAGGGTTA-5'
 ← -

Fig. 27F

- →
 5' -GCGTANXYZZAAGTGCGAACGQQXYCTTCGTCCCAAT-3'
 3' -CGCATNYXQQTTCACGCTTGCZZZYXGAAGCAGGGTTA-5'
 ← -UL9- - ← -

Fig. 27G

- →
 5' -GCGTANQQXYAAGTGCGAACGXYZZCTTCGTCCCAAT-3'
 3' -CGCATNZZYXTTCACGCTTGCYXQQGAAGCAGGGTTA-5'
 ← - ← UL9- -

Fig. 27H

HIVBH101 (HIV LTR sequence)
 GTTAGAGTGGAGGTTTGACAGCCGCCTAGCATTTCATCACATGGCCCGAG
 AGCTGCATCCGGAGTACTTCAAGAACTGCTGACATCGAGCTTGCTACAAG
 <<NF-κB>> <<NF-κB>> <Sp-1 III> <Sp-1 II>
 GGACTTTCCGCTGGGGACTTTCCAGGGAGGCGTGGCCTGGGCGGGACTGG
 Sp-1 II> TATA
 GGAGTGGCGAGCCCTCAGATCCTGCATATAAGCAGCTGCTTTTTGCCTGT
 +1 prim transcript start →
 ACTG GGTCTCTCTGGTTAGACCAGATCTGAGCCTGGGAGCTC

Fig. 28

EcoRI/PstI
 primer
 5' -GCAGAATTCTGCAG-3' UL9 site
 5' -GCAGAATTCTGCAG(N)_xCGTTCGCACTTTCTAGAGCTCAGG-3'
 3' -CGTCTTAAGACGTC(N)_xGCAAGCGTGAAAGATCTCGAGTCC-5'
 test site 3' -AGATCTCGAGTCC-5'
 XbaI/SacI
 primer

where X is the number of bases in the test site.

Fig. 29A

5' -GCAGAATTCTGCAGNNNNCGTTCGCACTTTCTAGAGCTCAGG-3'

Fig. 29B

5' -GCAGAATTCTGCAGNNNNNNNNCGTTCGCACTTTCTAGAGCTCAGG-3'

Fig. 29C

5' -GCAGAATTCTGCAGCGTTCGCACTTNNNNNNNTCTAGAGCTCAGG-3'

Fig. 29D

UL9 Site 3' relative to the test sequence:

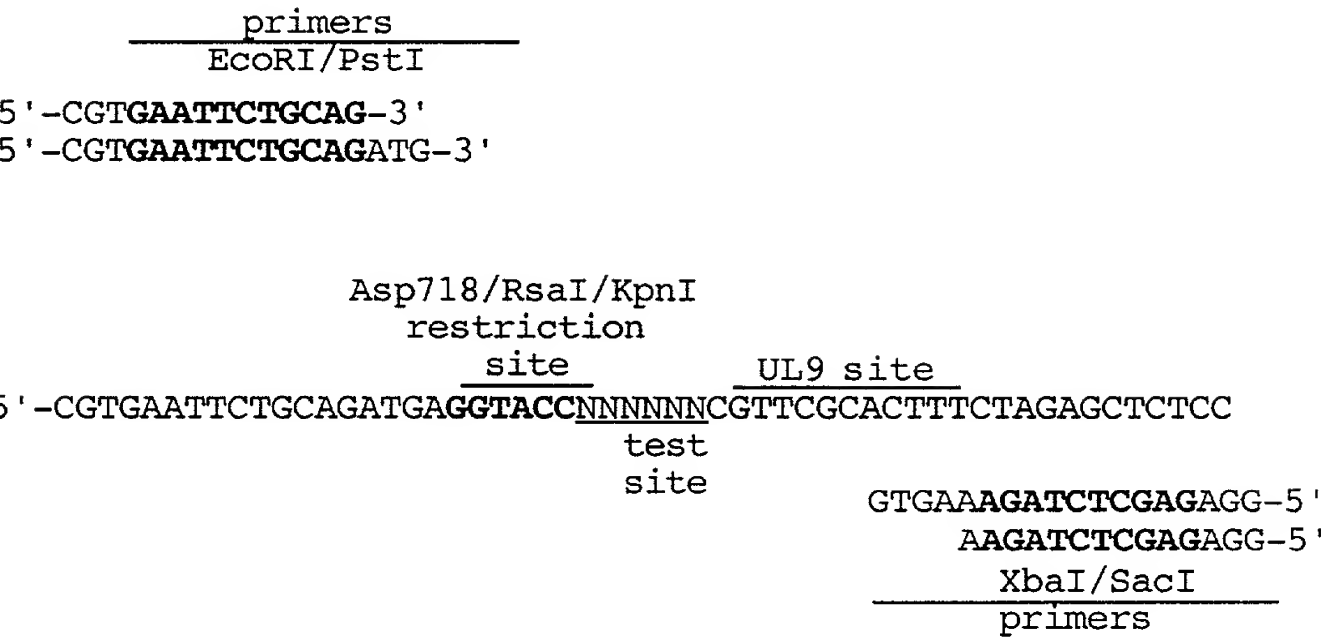


Fig. 30

Small Molecule Binding Sequence	Expected Score in Assay	Potential Test Site Sequence
UL9 site		
5'-...CGTTCGCACTTTTAC...-3'	high	TTAC
5'-...CGTTCGCACTTTACN...-3'	high	TACN
5'-...CGTTCGCACTTACNN...-3'	high	ACNN

Fig. 31

Small Molecule Binding Sequence	Expected Score in Assay	Potential Test Site Sequence
SmaI		
5'-...CCCGGGTTAC...-3'	high	TTAC
5'-...CCCGGGTACN...-3'	low	TACN
5'-...CCCGGGACNN...-3'	low	ACNN

Fig. 32